

Qy 181 AAGCAGAGCCTGCTGTTTCTGTTCTGTAAGTCTGTTCAGAGTATCATTCGTTGTTG 240
Db 181 AAGCAGAGCCTGCTGTTTCTGTTCTGTAAGTCTGTTCAGAGTATCATTCGTTGTTG 240
Qy 241 GAGTGTGAGTCTTCTTCAAGTCTCTCAAGCGTCACTTACTACTACTATGACT 300
Db 241 GAGTGTGAGTCTTCTTCAAGTCTCTCAAGCGTCACTTACTACTACTATGACT 300
Qy 301 CCAGAGAGTATAGAGAGTGGGATCTTCCTGTTATTAACCTATAGTTCCTCCGCT 360
Db 301 CCAGAGAGTATAGAGAGTGGGATCTTCCTGTTATTAACCTATAGTTCCTCCGCT 360
Qy 361 TAGCGTAGGCTCTTCTCTGCTCTGCTAAGAGATGGGCTCTCGTCAAGCGTGAAGCT 420
Db 361 TAGCGTAGGCTCTTCTCTGCTCTGCTAAGAGATGGGCTCTCGTCAAGCGTGAAGCT 420
Qy 421 AACCGTCCAAAAAAGAACGCTAAGCTCTGAGAGCTCCG 458
Db 421 AACCGTCCAAAAAAGAACGCTAAGCTCTGAGAGCTCCG 458

RESULT 2
AX685342 458 bp DNA linear PAT 29-MAR-2003
LOCUS
DEFINITION Sequence 2 from Patent WO02095021.
ACCESSION AX685342
VERSION AX685342.1 GI:29371665
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE
1. 458
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic ROS optimized for plant codon usage and encoding fusion of ROS and nuclear localization signal"

ORIGIN
1
Hannoufa, A., Hegedus, D. and Bate, N.
A repressor-mediated regulation system for control of gene expression in plants
Patent: WO 02095021-A 2 28-NOV-2002;
The Minister of Agriculture and Agri-Food Canada (CA)
Location/Qualifiers

Qy 1 ATGACTGAGACTGCTTACCGTAAGCTCAAGATCTTCTGTTGAGCTTACGCTGATATC 60
Db 1 ATGACTGAGACTGCTTACCGTAAGCTCAAGATCTTCTGTTGAGCTTACGCTGATATC 60
Qy 61 GTTGCTGCTTACGTTTCTTCAACAGTGTGTTCTGTTACTGAGCTTCTGAGCTTATCT 120
Db 61 GTTGCTGCTTACGTTTCTTCAACAGTGTGTTCTGTTACTGAGCTTCTGAGCTTATCT 120
Qy 121 GATGTTCACTGCACTTCTGGAACATCTGCTCTGCTTCTGTTGCTGTTAACGTTGAG 180
Db 121 GATGTTCACTGCACTTCTGGAACATCTGCTCTGCTTCTGTTGCTGTTAACGTTGAG 180
Qy 181 AAGAGAGAGCTGCTGTTTCTGTTGTAAGTCTGTTAAGATGATGATGATGTTGTTG 240
Db 181 AAGAGAGAGCTGCTGTTTCTGTTGTAAGTCTGTTAAGATGATGATGATGTTGTTG 240
Qy 241 GAGTGTGAGTCTTCTTCAAGTCTCTCAAGCGTCACTTACTACTACTATGACT 300
Db 241 GAGTGTGAGTCTTCTTCAAGTCTCTCAAGCGTCACTTACTACTACTATGACT 300
Qy 301 CCAAGAGAGTATAGAGAGAGTGGATCTTCTGTTGATTAACCTATAGTTCCTGCT 360
Db 301 CCAAGAGAGTATAGAGAGAGTGGATCTTCTGTTGATTAACCTATAGTTCCTGCT 360

Query Match 100.0%; Score 458; DB 2; Length 458;
Best Local Similarity 100.0%; Pred. No. 1.2e-129;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 301 CCAGAGAGTATAGAGAGAGTGGGATCTTCTGTTGATTAACCTATAGTTCCTGCT 360
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Db 361 TAGCGTAGGCTCTTCTCTGCTCTGCTAAGAGATGGGCTCTCGTCAAGCGTGAAGCT 420
Qy 421 AACCGTCCAAAAAAGAACGCTAAGCTCTGAGAGCTCCG 458
Db 421 AACCGTCCAAAAAAGAACGCTAAGCTCTGAGAGCTCCG 458

RESULT 3
AX963308 472 bp DNA linear PAT 14-JAN-2004
LOCUS
DEFINITION Sequence 2 from Patent WO03104462.
ACCESSION AX963308
VERSION AX963308.1 GI:40882061
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE
1. 472
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic ROS"

ORIGIN
1
Hannoufa, A., Lydiatte, D.J. and Gao, M.J.
Regulation of gene expression using chromatin remodeling factors
Patent: WO 03104462-A 2 18-DEC-2003;
Her Majesty The Queen in Right of Canada, as represented; by The Minister of Agriculture and Agri-Food Canada (CA)
Location/Qualifiers

Qy 1 ATGACTGAGACTGCTTACCGTAAGCTCAAGATCTTCTGTTGAGCTTACGCTGATATC 60
Db 15 ATGACTGAGACTGCTTACCGTAAGCTCAAGATCTTCTGTTGAGCTTACGCTGATATC 74
Qy 61 GTTGCTGCTTACGTTTCTTCAACAGTGTGTTCTGTTACTGAGCTTCTGAGCTTATCT 120
Db 75 GTTGCTGCTTACGTTTCTTCAACAGTGTGTTCTGTTACTGAGCTTCTGAGCTTATCT 134
Qy 121 GATGTTCACTGCACTTCTGGAACATCTGCTCTGCTTCTGTTGCTGTTAACGTTGAG 180
Db 135 GATGTTCACTGCACTTCTGGAACATCTGCTCTGCTTCTGTTGCTGTTAACGTTGAG 194
Qy 181 AAGCAGAGCCTGCTGTTTCTGTTGTAAGTCTGTTAAGATGATGATGATGTTGTTG 240
Db 195 AAGCAGAGCCTGCTGTTTCTGTTGTAAGTCTGTTAAGATGATGATGATGTTGTTG 254
Qy 241 GAGTGTGAGTCTTCTTCAAGTCTCTCAAGCGTCACTTACTACTACTATGACT 300
Db 255 GAGTGTGAGTCTTCTTCAAGTCTCTCAAGCGTCACTTACTACTACTATGACT 314
Qy 301 CCAGAGAGTATAGAGAGAGTGGGATCTTCTGTTGATTAACCTATAGTTCCTGCT 360
Db 315 CCAGAGAGTATAGAGAGAGTGGGATCTTCTGTTGATTAACCTATAGTTCCTGCT 374
Qy 361 TAGCGTAGGCTCTTCTCTGCTCTGCTAAGAGATGGGCTCTCGTCAAGCGTGAAGCT 420
Db 375 TAGCGTAGGCTCTTCTCTGCTCTGCTAAGAGATGGGCTCTCGTCAAGCGTGAAGCT 434
Qy 421 AACCGTCCAAAAAAGAACGCTAAGCTCTGAGAGCTCCG 458
Db 435 AACCGTCCAAAAAAGAACGCTAAGCTCTGAGAGCTCCG 472

RESULT 4

AX958630	LOCUS	AX958630	447 bp	DNA	linear	PAT 14-JAN-2004
AX958630	DEFINITION	Sequence 3 from Patent WO03100063.				
AX958630	ACCESSION	AX958630				
AX958630	VERSION	AX958630.1 GI:40879470				
AX958630	KEYWORDS	.				
AX958630	SOURCE	synthetic construct				
AX958630	ORGANISM	other sequences; artificial sequences.				
AX958630	REFERENCE	1				
AX958630	AUTHORS	Hannoufa, A., Hegedus, D. and Bate, N.				
AX958630	TITLE	A repressor-mediated regulation system for control of gene expression in plants				
AX958630	JOURNAL	Patent: WO 03100063-A 3 04-DEC-2003;				
AX958630	FEATURES	Her Majesty The Queen in Right of Canada, as Represented, by The Minister of Agriculture and Agri-Food (CA)				
AX958630	source	Location/Qualifiers				
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AX958630	source	/organism="synthetic construct"				
AX958630	source	/mol_type="unassigned DNA"				
AX958630	source	/db_xref="taxon:32630"				
AX958630	source	/note="ROS consensus sequence"				
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AX958630	Query Match	69.2%; Score 317; DB 2; Length 447;				
AX958630	Best Local Similarity	58.3%; Pred. No. 3.3e-86;				
AX958630	Matches 260; Conservative	97; Mismatches 89; Indels 0; Gaps 0;				
AX958630	Oy	1 ATGACTGAGCTGCTTACCGTAAAGCTGCTTCTTGTGAGCTTACTGATGATTC 60				
AX958630	Db	1 ATGACNGRACACGCTTAAGNAAACNCARGAAYTYNTGNTGARITYTACNGCNGAYATH 60				
AX958630	Oy	61 GTTGCTGCTTACGTTTCTAACCAAGCTGTTCTCTGTACTGAGCTTCTGGAATTATCTCT 120				
AX958630	Db	61 GTNGCNGCNTAYGTWMSNAAVCAYGTGNTGNCNGTACNGARITYTACNGAYTNAHTMSN 120				
AX958630	Oy	121 GATGTTCTACTGCACCTTTCTGGAACATCTGCTCTGCTTCTGTTGCTGTTAAGTTGAG 180				
AX958630	Db	121 GAYGTCNCAVCACNGCYTWTMSNGNACNMSNGNCNCGNMSGTGNCNGTAAAYGTNGAR 180				
AX958630	Oy	181 AAGCAGAGCCTGCTGTTCTGTTGCTGAAGTCTGTTAGATGATCATATGCTTGTGTTG 240				
AX958630	Db	181 AARCARARCCNGCNGTWTMSNTGNAARMSNGTNCARGAAYCAATHTGTTGTYTN 240				
AX958630	Oy	241 GAGTGTGTTGCTTCTTCAAGTCTCTCAAGCTCACTTACTACTCATCTATGACT 300				
AX958630	Db	241 GARTGTGNGGMSWSTTYAARNSYTNABRMNCAYTYTNACACACACAYMSNATGACN 300				
AX958630	Oy	301 CCAGAGGAGTATAGAGAGAGTGGGATCTTCTGTGATTAACCTATGTTGCTCTGCT 360				
AX958630	Db	301 CCNGRARGARTAYMGNGARAAARATGGGAYTYTNCNMGNTGAYTAYCCNATGTGNCNCNCGN 360				
AX958630	Oy	361 TACGCTGAGGCTCGTTCCTGCTGCTGCTAAGAGATGGGCTTCGCTACCGTCGTAAAGCT 420				
AX958630	Db	361 TAYGCGNARGCNCMGMSWMSNGTNTNCNARGARARATGGGAYTYTNGCARMNGNMAHRCN 420				
AX958630	Oy	421 AACCGTCCAAAAAAGAACGTAAGT 446				
AX958630	Db	421 AAYMGNCCNAPARAPARAPAMGNARGT 446				
AX958630	RESULT 5					
AX958630	LOCUS	AX963309 447 bp DNA linear PAT 14-JAN-2004				
AX958630	DEFINITION	Sequence 3 from Patent WO03104462.				
AX958630	ACCESSION	AX963309				
AX958630	VERSION	AX963309.1 GI:40882062				
AX958630	KEYWORDS	.				
AX958630	SOURCE	synthetic construct				
AX958630	ORGANISM	synthetic construct				
AX958630	REFERENCE	other sequences; artificial sequences.				
AX958630	AUTHORS	1 Hannoufa, A., Lydiate, D. J. and Gao, M. J.				

TITLE		Regulation of gene expression using chromatin remodelling factors									
JOURNAL		Patent: WO 03104462-A 3 18-DEC-2003.									
		Her Majesty The Queen in Right of Canada, as represented: by The Minister of Agriculture and Agri-Food Canada (CA)									
FEATURES		Location/Qualifiers									
source		1..447									
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misc_feature		1..447									
		/note="where n is #a# or #c# or #t# or #g#"									
ORIGIN											
Query Match		69.2%; Score 317; DB 2; Length 447;									
Best Local Similarity		58.3%; Pred. No. 3.3e-86;									
Matches 260; Conservative		97; Mismatches 89; Indels 0; Gaps 0;									
QY	1	ATGACTGAGACTGTTACGGTAAACGCTCAGAGATCTTCTGTGTGAGCTTACTGATATC	60								
DB	1	ATGACGAGACGAGTATGAGAAAGCAGAGATCTTGTGTGAGCTTACTGATATC	60								
QY	61	GTTCCTCTTACCTTTCTTCAACACAGTGTCTGTCTGACTGAGCTTCTGACTTATCT	120								
DB	61	GTTCGCTGCTTATGAGTATGAGAAAGCAGAGATCTTGTGTGAGCTTACTGATATC	120								
QY	121	GATGTTCAATCTGACTTTCTGGAACATCTGCTCTTCTGTGCTGTTAACGTTGAG	180								
DB	121	GATGCTGCTTATGAGTATGAGAAAGCAGAGATCTTGTGTGAGCTTACTGATATC	180								
QY	181	AAGCAGAAAGCTGTGTTTCTGTTCCGTAAGTCTGTTAGATGATCATTCGTTGTTG	240								
DB	181	AATCAGAAAGCTGTGTTTCTGTTCCGTAAGTCTGTTAGATGATCATTCGTTGTTG	240								
QY	241	GAGTGTGTGTTCTTCTTCAAGTCTCTCAAGGTCACCTTACTACTCATCTATGACT	300								
DB	241	GAGTGTGTGTTCTTCTTCAAGTCTCTCAAGGTCACCTTACTACTCATCTATGACT	300								
QY	301	CCAGAGAGATATAGAGAAAGTGGATCTTCTGTGTTATTACCTTATGTTGCTCTGCT	360								
DB	301	CCAGAGAGATATAGAGAAAGTGGATCTTCTGTGTTATTACCTTATGTTGCTCTGCT	360								
QY	361	TACCTGAGGCTGCTTCTCTGTTCTGCTTAAAGATGGTCTCGGTACGCTGTAAGCT	420								
DB	361	TACCTGAGGCTGCTTCTCTGTTCTGCTTAAAGATGGTCTCGGTACGCTGTAAGCT	420								
QY	421	AACGCTCAAAAAAGAACGCTAAGT	446								
DB	421	AATGCTCAAAAAAGAACGCTAAGT	446								
RESULT 6											
LOCUS		AX685343 447 bp DNA linear PAT 29-MAR-2003									
DEFINITION		Sequence 3 from Patent WO02095021.									
ACCESSION		AX685343									
VERSION		AX685343.1 GI:29371666									
KEYWORDS											
SOURCE		.									
ORGANISM		synthetic construct									
REFERENCE		synthetic construct									
AUTHORS		other sequences; artificial sequences.									
TITLE		1									
JOURNAL		Hannoufa, A., Hegedus, D. and Bate, N.									
		A repressor-mediated regulation system for control of gene									
		expression in plants									
		Patent: WO 02095021-A 3 28-NOV-2002;									
		The Minister of Agriculture and Agri-Food Canada (CA)									
FEATURES		Location/Qualifiers									
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		/db_xref="taxon:32630"									
		/note="Composite ROS Sequence"									
		/note="where n is #a# or #c# or #t# or #g#"									

ORIGIN

Query Match 59.2%; Score 317; DB 2; Length 447;

Best Local Similarity 58.3%; Pred. No. 3.3e-86; Mismatches 89; Indels 0; Gaps 0;

Matches 260; Conservative 97; Mismatches 89; Indels 0; Gaps 0;

QY 1 ATGACTGAGACTGCTTACCGTAAACGCTCAGAGATCTTCTGTTGAGCTTACTGCTGATATC 60
DB 1 ATGACNBARACNCGNTAYGNAAYGCNCARGAAYTNTGNTGARYTNACNCGNAGATH 60
QY 61 GTTGCTGCTTACGTTTCTTAACCAAGTGTTCCTGTTACTGAGCTTCTGCACTTATCTCT 120
DB 61 GTTGCGNCGNTAYGNTMNAAYCAVGTGTCNCGTNAACNARYTNCNCGNATNATHMSN 120
QY 121 GATGTCATCTGCACTTCTGGAACATCTGCTCTCTCTCTGTTGCTGTTAAGCTGAG 180
DB 121 GATGTCNAYACNCGNTYTNMNGNACNWSNCGNCGNCGNNGTNGCNNAAYGTNGAR 180
QY 181 AAGCAGAAGCTGCTGTTTCTGTTCTGTTAGTCTGTTGAGATGATCATCTGTTGTTTG 240
DB 181 AAGCAGARARCCNCGNCGNTMNGNAAHMSNCGTNCARGAAYCAVATHGTTGTYTN 240
QY 241 GAGTGTGTGCTTCTTCAAGTCTCTCAAGGCTCACTTACTACTCATCTATGACT 300
DB 241 GAGTGTGNGNMSNTTYAARMSYTNAAHMGNCAYTNAACNACNCAVCAWMSNATGACN 300
QY 301 CCAGAGAGATATAGAGAAGTGGATCTTCTGTTGATTACCTATGCTGCTGCT 360
DB 301 CCNAGARARATYMGNGARBARATGGGAYTTCNCGTNAAYTACNATGTCNCGNCGN 360
QY 361 TAGCTGAGGCTGCTTCTGCTCTGCTTAAGAGATGGTCTCGTCAAGCTGTAAGCT 420
DB 361 TAGCNGARCCNCGNCGNTMNGNAYTNGCNAARGARATGAGNTNGNCARMGNGMAARGCN 420
QY 421 AACCGTCAAAAAAAGCGTAAAGT 446
DB 421 AATMGNCNARARARARARMGNAAGT 446

RESULT 7

LOCUS AX958628 429 bp DNA linear PAT 14-JAN-2004
DEFINITION Sequence 1 from Patent WO03100063.
ACCESSION AX958628
VERSION AX958628.1 GI:40879468

KEYWORDS Agrobacterium tumefaciens (Rhizobium radiobacter)
SOURCE Agrobacterium tumefaciens
ORGANISM Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Agrobacterium.

REFERENCE 1
AUTHORS Hannoufa, A., Hegedus, D. and Bate, N.
TITLE A repressor-mediated regulation system for control of gene
JOURNAL expression in plants
Patent: WO 03100063-A 1 04-DEC-2003;
Her Majesty the Queen in Right of Canada, as Represented; by The
Minister of Agriculture and Agri-Food (CA)

FEATURES
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/organism="Agrobacterium tumefaciens"
/mol_type="unassigned DNA"
/db_xref="taxon:358"

ORIGIN

Query Match 63.7%; Score 291.6; DB 2; Length 429;

Best Local Similarity 80.3%; Pred. No. 2.2e-78; Mismatches 84; Indels 0; Gaps 0;

Matches 342; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1 ATGACTGAGACTGCTTACCGTAAACGCTCAGAGATCTTCTGTTGAGCTTACTGCTGATATC 60
DB 1 ATGACGGAACCTGATACGATACGCAAGATCTGCTGTCGACATGACGCGGAGATAT 60
QY 61 GTTGCTGCTTACGTTTCTTAACCAAGTGTTCCTGTTACTGAGCTTCTGCACTTATCTCT 120

DB 61 GTTGCTGCTTACGTTTCTTAACCAAGTGTTCCTGTTACTGAGCTTCTGCACTTATCTCT 120
QY 121 GATGTCATACGCACTTCTGGAACATCTGCTCTGCTTCTGTTGAGCTTAAAGCTTAAAG 180
DB 121 GATGTCATACGCACTGACGCGGAACATCGGACCGGATCGGTGCGGCAATGTGAA 180
QY 181 AAGCAGAAGCTGCTTCTGTTCTGTTAGTCTGTTCAAGATGATCATATCGTTGTTTG 240
DB 181 AAGCAGAACCTGCTGCTGTTCTGTTAGTCTGTTCAAGATGATCATATCGTTGTTTG 240
QY 241 GAGTGTGTGCTTCTTCAAGTCTCTCAAGGCTCACTTACTACTCATCTATGACT 300
DB 241 GAATGTGTGCTGCTGTTCAAGTCTCAACGCGCATGACGACATCAACAGATGACG 300
QY 301 CCAGAGAGATATAGAGAAGTGGATCTTCTGTTGATTACCTATGCTGCTGCT 360
DB 301 CCGAAGAAATATCGCAAAAATGGGATCTGCGGATGATTTATCATGTTGTTCCGCC 360
QY 361 TAGCTGAGGCTGCTTCTGCTCTGCTTAAGAGATGGTCTCGTCAAGCTGTAAGCT 420
DB 361 TAGCCGAAGCCGCTTCTGCGGCTCGCCAGGAATGGTCTCGTCAAGCGCGCAAGGCG 420
QY 421 AACCGT 426
DB 421 AACCGT 426

RESULT 8

LOCUS AX685341 429 bp DNA linear PAT 29-MAR-2003
DEFINITION Sequence 1 from Patent WO02095021.
ACCESSION AX685341
VERSION AX685341.1 GI:29371664

KEYWORDS Agrobacterium tumefaciens (Rhizobium radiobacter)
SOURCE Agrobacterium tumefaciens
ORGANISM Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Agrobacterium.

REFERENCE 1
AUTHORS Hannoufa, A., Hegedus, D. and Bate, N.
TITLE A repressor-mediated regulation system for control of gene
JOURNAL expression in plants
Patent: WO 02095021-A 1 28-NOV-2002;
The Minister of Agriculture and Agri-Food Canada (CA)

FEATURES
source 1..429
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/db_xref="taxon:358"

ORIGIN

Query Match 63.7%; Score 291.6; DB 2; Length 429;

Best Local Similarity 80.3%; Pred. No. 2.2e-78; Mismatches 84; Indels 0; Gaps 0;

Matches 342; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1 ATGACTGAGACTGCTTACCGTAAACGCTCAGAGATCTTCTGTTGAGCTTACTGCTGATATC 60
DB 1 ATGACGGAACCTGATACGATACGCAAGATCTGCTGTCGACATGACGCGGAGATAT 60
QY 61 GTTGCTGCTTACGTTTCTTAACCAAGTGTTCCTGTTACTGAGCTTCTGCACTTATCTCT 120
DB 61 GTTGCTGCTTACGTTTCTTAACCAAGTGTTCCTGTTACTGAGCTTCTGCACTTATCTCT 120
QY 121 GATGTCATACGCACTTCTGGAACATCTGCTCTGCTTCTGTTAAGCTGTTAG 180
DB 121 GATGTCATACGCACTGACGCGGAACATCGGACCGGATCGGTGCGGCAATGTGAA 180
QY 181 AAGCAGAAGCTGCTTCTGTTCTGTTAGTCTGTTCAAGATGATCATATCGTTGTTTG 240
DB 181 AAGCAGAAGCTGCTTCTGTTCTGTTAGTCTGTTCAAGATGATCATATCGTTGTTTG 240
QY 241 GAGTGTGTGCTTCTTCAAGTCTCTCAAGGCTCACTTACTACTCATCTATGACT 300

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Db      241 GAATGTGATGCTGTTCAAGTCCCTCAAAACGCACTGACGACGATCAGAGATACG 300
Qy      301 CCAGAGAGATATAGAGAAATGGGATCTTCTGTTGATTAACCTATGTTGCTCTGCT 360
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Qy      361 TACGCTAGAGCTGTTCTGCTCTGCTTAAGAGATGGGCTCGGTCAGCGTCTGAAGCT 420
Db      361 TATGCCAAGCCCGCTGCGGCTCGCAAGAAATGGGCTCGGTCAGCGCGCGAAGCGC 420
Qy      421 AACCGT 426
Db      421 AACCGT 426

RESULT 9
ATTUROS 1468 bp DNA linear BCT 26-APR-1993
DEFINITION A.tumefaciens ros gene, complete cds.
ACCESSION M65201
VERSION M65201.1 GI:142274
KEYWORDS ros gene.
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Agrobacterium tumefaciens; Rhizobium radiobacter;
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Agrobacterium.
REFERENCE 1 (bases 1 to 1468)
AUTHORS Cooley,M.B., D'Souza,M.R. and Kado,C.I.
TITLE The virC and virD operons of the Agrobacterium Ti plasmid are
regulated by the ros chromosomal gene: analysis of the cloned ros
gene
JOURNAL J. Bacteriol. 173 (8), 2608-2616 (1991)
PUBMED 2013576
COMMENT Original source text: A.tumefaciens DNA.
FEATURES
location/Qualifiers
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82..87
/gene="ros"
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-10_signal 105..110
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/note="putative; putative"
gene order(189..197,202..210)
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repeat_region /function="autoregulation repressor binding site"
repeat_unit 189..197
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repeat_unit 202..210
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CDS 309..737
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recorded"
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misc_feature 542..595
/note="zinc finger; putative; putative"
/function="DNA binding"

ORIGIN
Query Match 63.7%; Score 291.6; DB 15; Length 1468;
Best Local Similarity 80.3%; Pred. No. 2e-78;
Matches 342; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy      1 ATGACTGAGACTGCTTAACGTTAAAGCTCAGATCTTCTGTTAGCTTACTGCTGATATC 60
Db      309 ATGACGGAATCTGCATACGGTAACGCCAGATCTGCTGATCGAATGACGGGATATT 368
Qy      61 GTTGCTGCTTACGTTCTTAACCAAGTTTCTCTGTTACTGAGCTTCTGACTTATCTCT 120
Db      369 GTGCTGCTTATGTAGCAACACGTTCTCCGTTAATGAGCTTCCCGGCTTATTTTCG 428
Qy      121 GATGTCATATCTACATCTTCTGACATCTGCTCTGCTTCTGTTGCTTTAAGTTAG 180
Db      429 GATGTTCAATCGGCACTACGCGAACAATCGGACCGGATCGGTGCGGTCATATTGTTGAA 488
Qy      181 AACGAGAAGCTGCTGTTTCTGTTCTGTTAAGTCTGTTCAAGATGATCATATCGTTTGTG 240
Db      489 AACGAGAAGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 548
Qy      241 GAATGTGATGCTTCTTCAAGTCTTCAAGCTTCACTTACTATCTATCTATGACT 300
Db      549 GAATGTGATGCTTCTTCAAGTCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCT 608
Qy      301 CCAGAGAGATATAGAGAAATGGGATCTTCTGTTGATTAACCTATGTTGCTCTGCT 360
Db      609 CCGGAAAGATATGCGGAAATGGGATCTGCGGTCATTAATCGATGTTGCTCCGCC 668
Qy      361 TACGCTAGAGCTGTTCTGCTCTGCTTAAGAGATGGGCTCGGTCAGCGTCTGAAGCT 420
Db      669 TATGCCAAGCCCGTTCGCGGCTCGCAAGAAATGGGCTCGGTCAGCGCGCGAAGCGC 728
Qy      421 AACCGT 426
Db      729 AACCGT 734

RESULT 10
AE008022 10212 bp DNA linear BCT 28-MAY-2004
LOCUS Agrobacterium tumefaciens str. C58 circular chromosome, section 80
DEFINITION of 254 of the complete sequence.
ACCESSION AE008022 AE007869
VERSION AE008022.1 GI:15155900
KEYWORDS Agrobacterium tumefaciens str. C58
SOURCE Agrobacterium tumefaciens str. C58
ORGANISM Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Agrobacterium.
REFERENCE 1 (bases 1 to 10212)
AUTHORS Hinkle,G., Slater,S.C. and Goodner,B.
TITLE Complete Genome Sequence of Agrobacterium tumefaciens C58
(Rhizobium radiobacter C58), the Causative Agent of Crown Gall
Disease in Plants
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 10212)
AUTHORS Hinkle,G., Slater,S.C. and Goodner,B.
TITLE Direct Submmission
JOURNAL Submitted (14-AUG-2001) Cereon Genomics, 45 Sidney Street,
Cambridge, MA 02139, USA
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location/Qualifiers
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gene

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Pseudomonas aeruginosa (strain PA01)"
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/transl_table=11
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/protein_id="AAK6711.1"
/db_xref="GI:15155901"
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Best Local Similarity 77.4%; Pred. No. 2.9e-72;
Matches 329; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

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Db 7716 GTTGCTCTTACGTTCTTAAACAGTGTCTCTGTTGAGCTTCTGACCTTATCTCT 7775
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Db 7776 GATGTCATCTGCACTTCTTGAACATCTGCTCTCTGTTGCTTTGATTAAGCTT 7835
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Qy 361 TACGCTAGAGCTCTTCTGCTGCTTAAGAGATGGTCTCGGTCAGCGTCGTAAGGCT 420
Db 8016 TATGCTCCAGAGCGCTGCTGCGGCTCGCCAAAGAAATGGTCTCGGTCAGCGTCGTAAGGCT 8075
Qy 421 AACCG 425
Db 8076 AGCCG 8080

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DEFINITION Agrobacterium tumefaciens str. C58 circular chromosome, section 82
ACCESSION AE009056 AE008688
VERSION AE009056.1 GI:17739283
KEYWORDS
SOURCE Agrobacterium tumefaciens str. C58
ORGANISM Agrobacterium tumefaciens str. C58

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REFERENCE
AUTHORS
1 (bases 1 to 10229)
Wood,D.W., Setubal,J.C., Kaul,R., Monks,D., Chen,L., Wood,G.E.,
Chen,Y., Woo,L., Kitajima,J.P., Okura,V.K., Almeida,N.F., Jr.,
Zhou,Y., Boyee,D., Sr., Chapman,P., Clendenning,J., Deatherage,G.,
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Krespan,M., Perry,M., Gordon-Kamm,B., Liao,L., Kim,S., Hendrick,C.,
Zhao,Z., Dolan,M., Tingey,S.V., Tomb,J., Gordon,M.P., Olson,M.V.,
and Nester,E.W.
The genome of the natural genetic engineer Agrobacterium
tumefaciens C58
Science 294 (5550) , 2317-2323 (2001)
11743193
JOURNAL
PUBMED
2 (bases 1 to 10229)
Wood,D.W., Setubal,J.C., Kaul,R., Monks,D., Chen,L., Wood,G.E.,
Chen,Y., Woo,L., Kitajima,J.P., Okura,V.K., Almeida,N.F., Jr.,
Zhou,Y., Boyee,D., Sr., Chapman,P., Clendenning,J., Deatherage,G.,
Gillet,W., Grant,C., Guenther,D., Kutyavin,T., Levy,R., Li,M.,
McClelland,E., Palmieri,A., Raymond,C., Rouse,G.,
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Karp,P., Romero,P., Zhang,S., Yoo,H., Tao,Y., Biddle,P., Jung,M.,
Krespan,M., Perry,M., Gordon-Kamm,B., Liao,L., Kim,S., Hendrick,C.,
Zhao,Z., Dolan,M., Tingey,S.V., Tomb,J., Gordon,M.P., Olson,M.V.,
and Nester,E.W.
Submitted (27-SEP-2001) Department of Microbiology, University of
Washington, 1959 NE Pacific Ave, Box 357242, Seattle, WA
98195-7242, USA
JOURNAL
PUBMED
11743193
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Best Local Similarity 77.4%; Pred. No. 2,9e-72;
Matches 329; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

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LOCUS A.radiobacter rosA gene.

DEFINITION X82941

ACCESSION X82941.1 GI:599612

VERSION X82941.1 GI:599612

KEYWORDS ros gene.

SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)

ORGANISM Agrobacterium tumefaciens (Rhizobium radiobacter); Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Agrobacterium.

REFERENCE 1

AUTHORS Brightwell,G., Hussain,H., Tiburtius,A., Yeoman,K.H. and Johnston,A.W.

TITLE Pleiotropic effects of regulatory ros mutants of Agrobacterium radiobacter and their interaction with Fe and glucose

JOURNAL Mol. Plant Microbe Interact. 8 (5), 747-754 (1995)

PUBMED 7579618

REFERENCE 2 (bases 1 to 783)

AUTHORS Hussain,H.A.

TITLE Direct Submission

JOURNAL Submitted (28-NOV-1994) H.A. Hussain, University of East Anglia, School of Biological Sciences, Norwich NR4 7TU, UK

FEATURES

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Qy 121 GATGTCATATCTGACTTTTCTGAACAATGCTCTCTGCTTCTGTGTGCTTAACGTTAG 180

Db 429 GATGTTACACGGGCTCACCGGAACGTCGCGCGGCATCGTAGGCTCAATGTTGAA 488

Qy 181 AAGCAGAACCTCTGTTTCTGTTTCGTAATCTGTTTACAGATGATATGTTGTTTG 240

Db 489 AAGCAGAACCGGCGCTCTGTCGCAAGTCGGTTAGAGACATATATGCTGTTTG 548

Qy 241 GAGTGTGCTGTTCTTCAAGTCTTCACGCTCACCTTACTACTATCTATGACT 300

Db 549 GAATGCGCGGCTCTTCAAGTCTCACGCGCATCTCAGACGATCACAGCATGACG 608

Qy 301 CCAGAGAGATATAGAGAGAGTGGATCTTCTTATTAACCTATAGTGTCTTCT 360

Db 609 CCGAAGAAATACCGCGAATAGGACCTCAGGTGATTAATCCGATGTTGCGCCGCC 668

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Qy 421 AACGTCGCAAAAAGAG 438

Db 729 AACGCTGATTTTCAAG 746

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DEFINITION Rhizobium leguminosarum bv. trifolii strain TAL transcriptional regulatory protein RosR (rosR) gene, complete cds.

ACCESSION AY683454

VERSION AY683454.1 GI:51012475

KEYWORDS

SOURCE Rhizobium leguminosarum bv. trifolii

ORGANISM Rhizobium leguminosarum bv. trifolii

REFERENCE 1

AUTHORS Janczarek,M.B. and Skorupska,A.

TITLE The exopolysaccharide production

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 856)

AUTHORS Janczarek,M.B. and Skorupska,A.

TITLE Direct Submission

JOURNAL Submitted (12-JUL-2004) General Microbiology, M. Curie-Sklodowska University, Akademicka 19, Lublin 20-033, Poland

FEATURES

source

1..856

/organism="Rhizobium leguminosarum bv. trifolii"

/mol_type="genomic DNA"

/strain="TAL"

/db_xref="taxon:386"

/note="biovar: trifolii"

124..555

/gene="rosR"

124..555

/gene="rosR"

CDS

124..555

/note="DNA binding protein: similar to Rhizobium etl1 RosR, Agrobacterium tumefaciens Ros and Sinorhizobium meliloti MucR; regulator of exopolysaccharide synthesis; member of Ros/MucR family of transcriptional regulators"

/codon_start=1

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/protein_id="AA092554.1"

/db_xref="GI:51012476"

/translation="MTDIATGNAPELVELTADIVAAYVSNHVPVSDLANLISDVHS ALSNTSVQPAALIVKOKPAVSVRKSDVDHIVCLECGNFKSLRHLMTTHSLSPE EYREKMDLPDYPMVAPAVAAEARSRLAKEMGLGQRKRG"

ORIGIN

Query Match 46.3%; Score 212.2; DB 15; Length 856;

Best Local Similarity 69.3%; Pred. No. 6.1e-54;
Matches 289; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

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DB 124 ATGACGATATAGGACCGAATGCGCCGAGCTGTTGTGAACTGACAGCCGACATC 183
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DB 244 GACGTGATTCGACACTGAGCAACACGTCCTGACCGAGCTGCTGGCGCATGTGAA 303
QY 181 AAGGAGAAGCTGCTGTTCTGTTCGTAAAGTCCTTGAAGATGATCATTCGTTGTTG 240
DB 304 AAGCAGAAGCTGAGTTTCTGTCCGCAAGTCCTTGAAGAGAGAGATCAGATCAGTTTG 363
QY 241 GAGTGTGATGCTTTCTTCAAGTCTCTCAAGGCTCAGCTTACTACTCATCTATGACT 300
DB 364 GAATGCGCGGCACTTCAAGTCTCTCAAGGCTCAGCTTACTACTCATCTATGACT 423
QY 301 CCAGAGAGATATAGAGAAAGTGGAATCTTCTGTGATTAACCTATGTTGCTCTGCT 360
DB 424 CCGGAAGATATCCGCGAAGATGGGACCTGCGCAGCATTAACCGATGTAGCCGCT 483
QY 361 TAGCTGAGGCTCTTCTCTCTCTGCTTAAGAGATGGTCTCGGTACAGCTGTAG 417
DB 484 TAGCCGAAGCGCTGCGCTGCGCTGCGCAAGATGGCGCTCGGCGAGCCGCAAG 540
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RESULT 14
AY683453 1174 bp DNA linear BCT 11-AUG-2004
DEFINITION Rhizobium leguminosarum bv. trifolii strain 24.1 transcriptional
regulatory protein RosR (rosR) gene, complete cds.
AY683453
AY683453.1 GI:51012473

LOCUS RME237844 432 bp DNA linear BCT 21-NOV-1999
DEFINITION Rhizobium meliloti mucr gene, strain BFB1.
AJ237844
AJ237844.1 GI:645845

ACCESSION RME237844
VERSION AJ237844.1
KEYWORDS mucr gene; MucR protein; transcriptional regulator.
SOURCE Sinorhizobium meliloti (Rhizobium meliloti)
ORGANISM Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium.

REFERENCE 1 (bases 1 to 1174)
Janczarek, M.B. and Skorupka, A.
rosR gene of Rhizobium leguminosarum bv. trifolii influencing on
the exopolysaccharide production
Unpublished

JOURNAL 2 (bases 1 to 1174)
Janczarek, M.B. and Skorupka, A.
REFERENCE
AUTHORS Janczarek, M.B. and Skorupka, A.
TITLE Submitted (12-JUL-2004) General Microbiology, M. Curie-Sklodowska
JOURNAL University, Akademicka 19, Lublin 20-033, Poland
location/Qualifiers

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SOURCE 1. 1174
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/strain="24.1"
/db_xref="taxon:386"
/note="biovar: trifolii"

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451..882
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CDS 451..882
/gene="rosR"
/note="DNA binding protein, similar to Rhizobium etli
RosR, Agrobacterium tumefaciens Ros and Sinorhizobium
meliloti MucR, regulator of exopolysaccharide synthesis;
member of Ros/MucR family of transcriptional regulators"
/codon_start=1
/transl_table=11
/product="transcriptional regulatory protein RosR"
/protein_id="AA192553.1"

/db_xref="GI:51012474"
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EYERKDLPIIDYPMVAPATAEASRLAKEMGLGRRKRG"

Query Match 46.3%; Score 212.2; DB 15; Length 1174;
Best Local Similarity 69.3%; Pred. No. 5.9e-54;
Matches 289; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

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ORIGIN
QY 1 ATGACTGAGACTGCTTACGCTTAACGCTCAGATATCTTCTGTGAGCTTACTGCTGATATC 60
DB 451 ATGACGATATAGGACCGAATGCGCCGAGCTGTTGTGAACTGACAGCCGACATC 510
QY 61 GTTGCTCTTACGTTTCTTAACCAAGTTTCTGTACTGAGTCTCTGAGCTTATCTCT 120
DB 511 GTCCGGCCCTATGTCAGAACCATGTTGTACCGGTACAGCACTGGCCATCTGATTTCC 570
QY 121 GATGTCATATCTGCACTTTCTGGAACATCTGCTCTGTTCTGTGCTTTAACTTGAG 180
DB 571 GAGGTGATTCGACACTGATTAACAGTCCGTACCGAGCTGCTGGCGCATGTGAA 630
QY 181 AAGCAGAAGCTGCTGTTTCTGTTCGTAAAGTCCTTGAAGATGATCATTCGTTGTTG 240
DB 631 AAGCAGAAGCTGCTGATTTCTGTCCGCAAGTCCTTGAAGAGAGATCAGATCAGATTTTG 690
QY 241 GAGTGTGATGCTTTCTTCAAGTCTCTCAAGGCTCAGCTTACTACTCATCTATGACT 300
DB 691 GAATGCGCGGCACTTCAAGTCTCTCAAGGCTCAGCTTACTACTCATCTATGACT 750
QY 301 CCAGAGAGATATAGAGAAAGTGGAATCTTCTGTGATTAACCTATGTTGCTCTGCT 360
DB 751 CCGGAAGATATCCGCGAAGATGGGACCTGCGCAGCATTAACCGATGTAGCCGCT 810
QY 361 TAGCTGAGGCTCTTCTCTCTCTGCTTAAGAGATGGTCTCGGTACAGCTGTAG 417
DB 811 TAGCCGAAGCGCTGCGCTGCGCTGCGCAAGATGGCGCTCGGCGAGCCGCAAG 867
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RESULT 15
RME237844

LOCUS RME237844 432 bp DNA linear BCT 21-NOV-1999
DEFINITION Rhizobium meliloti mucr gene, strain BFB1.
AJ237844
AJ237844.1 GI:645845

ACCESSION RME237844
VERSION AJ237844.1
KEYWORDS mucr gene; MucR protein; transcriptional regulator.
SOURCE Sinorhizobium meliloti (Rhizobium meliloti)
ORGANISM Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium.

REFERENCE 1
Martin, M., Lloret, J., Sanchez-Contreras, M., Bonilla, I. and
Rivilla, R.
MucR does not repress expB genes expression in a galactoglucan
producing Sinorhizobium meliloti
Unpublished

JOURNAL 2 (bases 1 to 432)
Rivilla, R.
REFERENCE
AUTHORS Rivilla, R.
TITLE Direct Submission
JOURNAL Submitted (20-APR-1999) Rivilla, R., Biología, Universidad Autónoma
de Madrid, Campus de Cantoblanco, Madrid 28049, SPAIN
location/Qualifiers

FEATURES
SOURCE 1. 432
/organism="Sinorhizobium meliloti"
/mol_type="genomic DNA"
/strain="BFB1"
/db_xref="taxon:382"
/country="Spain"

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CDS 1..432
/gene="mucR"
/function="putative transcriptional regulator"

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FT      /*tag= a
XX      /note= "Nuclear localisation signal peptide"
PN      WO200295021-A2.
XX      28-NOV-2002.
PD      23-MAY-2002; 2002WO-CA000740.
XX      23-MAY-2001; 2001US-0292973P.
PR      (MIAC ) CANADA DEPT AGRIC & AGRI-FOOD CANADA.
XX      Hannoufa A, Hegedus D, Bate N;
XX      WPI; 2003-148467/14.
XX      New nucleic acid molecule encoding a ROS repressor, useful for
PT      controlling gene expression in plants, comprises a regulatory region
PT      operatively linked to a gene of interest and one or more ROS operator
PS      sequence.
XX      Disclosure; Fig 1B; 84pp; English.
XX      The present invention relates to a novel nucleic acid molecule encoding a
CC      ROS repressor protein optimised for plant codon usage and exhibiting ROS
CC      operator binding activity and/or ROS repressor activity. The nucleic acid
CC      molecule comprises a regulatory region operatively linked to a gene of
CC      interest and one or more ROS operator sequence capable of controlling the
CC      activity in controlling gene expression in plants using a repressor protein
CC      and corresponding operator sequences. The present sequence is
CC      Agrobacterium tumefaciens ros repressor codon optimised DNA
XX      SQ
XX      Sequence 472 BP; 92 A; 110 C; 117 G; 153 T; 0 U; 0 Other;
XX      Query Match      100.0%; Score 458; DB 8; Length 472;
XX      Best Local Similarity 100.0%; Pred. No. 2.7e-121;
XX      Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      1 ATGACTGAGACTGCTTACGCTTAACGCTCAAGATCTTCTGTTGAGCTTACTGATATC 60
DB      15 ATGACTGAGACTGCTTACGCTTAACGCTCAAGATCTTCTGTTGAGCTTACTGATATC 74
XX      61 GTTGCTCTTACGCTTCTTAACGCTTGTCTGTTAAGCTTCTGGAATTATCTCT 120
DB      75 GTTGCTCTTACGCTTCTTAACGCTTGTCTGTTAAGCTTCTGGAATTATCTCT 134
XX      121 GATGTTCAATCTGACCTTTCTGGAACATCTGCTCTGCTTCTGTTGCTTTAAAGCTT 180
DB      135 GATGTTCAATCTGACCTTTCTGGAACATCTGCTCTGCTTCTGTTGCTTTAAAGCTT 194
XX      181 AAGCAGAAAGCTGCTGTTTCTGTTGTAAGCTGTTGAGATGATCATATGTTGTTT 240
DB      195 AAGCAGAAAGCTGCTGTTTCTGTTGTAAGCTGTTGAGATGATCATATGTTGTTT 254
XX      241 GAGTGTGTGTTCTTTCAAGCTCTCAAGGCTCACTTACTACTCATATGATGACT 300
DB      255 GAGTGTGTGTTCTTTCAAGCTCTCAAGGCTCACTTACTACTCATATGATGACT 314
XX      301 CCAAGAGAGTTAAGAGAAAGTGGGATCTTCTGTTGATTAACCTTAAGTGTCTCCGCT 360
DB      315 CCAAGAGAGTTAAGAGAAAGTGGGATCTTCTGTTGATTAACCTTAAGTGTCTCCGCT 374
XX      361 TACGCTGAGGCTCGTTCTCGTCTGCTAAGAGATGGGCTCGGCTCAAGCGTGTAAAGGCT 420
DB      375 TACGCTGAGGCTCGTTCTCGTCTGCTAAGAGATGGGCTCGGCTCAAGCGTGTAAAGGCT 434
XX      421 AACCGTCCAAAAAAGAACGCTAAGGCTGTAGAGCTCGC 458
DB      435 AACCGTCCAAAAAAGAACGCTAAGGCTGTAGAGCTCGC 472

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RESULT 4
AD114224
ID AD114224 standard; DNA; 472 BP.
XX
XX AD114224;
AC
XX
XX 22-APR-2004 (first entry)
DT
XX
XX Plant codon optimised Agrobacterium tumefaciens ROS DNA Segid 2.
DE
XX
XX ROS; ds; gene; transgenic plant; chromatin remodelling factor;
XX DNA binding protein; VP16; GAL4; recruitment factor; BnSCL1; BnKCP1;
XX histone acetyl transferase; HAT; histone deacetylase; HD; HDA; HDAC;
XX HDAl9; cold tolerance.
XX Agrobacterium tumefaciens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH 15..464
FT CDS /*tag= a
PT /product= "Plant codon optimised ROS protein"
XX
XX WO2003104462-A2.
XX
XX 18-DEC-2003.
XX
XX 06-JUN-2003; 2003WO-CA000822.
XX
XX 06-JUN-2002; 2002US-0387088P.
XX
XX (MIAC ) CANADA DEPT AGRIC & AGRI-FOOD CANADA.
XX Hannoufa A, Lydiata DJ, Gao M;
XX WPI; 2004-062364/06.
XX DR P-PSDB; AD114226.
XX
XX Regulating expression of a nucleic acid sequence of interest by providing
XX a eukaryote and growing the eukaryote.
XX
XX Example 1; SEQ ID NO 2; 178pp; English.
XX
XX This invention relates to a novel method for regulating gene expression
CC in transgenic plants using chromatin remodelling factors. Specifically,
CC it comprises transforming a plant with one or more constructs comprising
CC a first nucleotide sequence that is operably linked to a regulatory
CC region and is capable of binding to a fusion protein, and a second
CC nucleotide sequence that encodes said fusion protein. This fusion protein
CC comprises a DNA binding protein (VP16 or GAL4), or a portion thereof,
CC that can bind to and regulate expression of the gene of interest (i.e.
CC the first polynucleotide) and a recruitment factor protein (BnSCL1 or
CC BnKCP1) that can bind to a chromatin remodelling protein. The present
CC invention describes the chromatin remodelling protein as a histone acetyl
CC transferase (HAT) or histone deacetylase (referred to as either HD, HDA
CC or HDAC), which is required to alter the structure of chromatin,
CC preferably this protein is HDAl9. As such, this method can be used to
CC alter plant characteristics and phenotype e.g. to increase cold tolerance
CC by regulating the expression of a nucleic acid sequence of interest. This
CC polynucleotide sequence is the Agrobacterium tumefaciens ROS DNA sequence
CC codon optimised for use in plants, used in an exemplification of the
CC invention.
XX
XX Sequence 472 BP; 92 A; 110 C; 117 G; 153 T; 0 U; 0 Other;
XX SQ
XX
XX Query Match      100.0%; Score 458; DB 12; Length 472;
XX Best Local Similarity 100.0%; Pred. No. 2.7e-121;
XX Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      1 ATGACTGAGACTGCTTACGCTTAACGCTCAAGATCTTCTGTTGAGCTTACTGATATC 60
DB      15 ATGACTGAGACTGCTTACGCTTAACGCTCAAGATCTTCTGTTGAGCTTACTGATATC 74

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QY 61 GTTGCTGCTTACGTTTCTAACCAAGTGTTCCTGTTACTAGAGCTTCTGACTTATCTCT 120
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 Db 75 GTTGCTGCTTACGTTTCTAACCAAGTGTTCCTGTTACTAGAGCTTCTGACTTATCTCT 134
 |||||
 QY 121 GATGTTCAATCTGACATTTCTTGAAACATCTGCTCTGCTTCTGTTGCTTTAAAGTTGAG 180
 |||||
 Db 135 GATGTTCAATCTGACATTTCTTGAAACATCTGCTCTGCTTCTGTTGCTTTAAAGTTGAG 194
 |||||
 QY 181 AACGAGAAGCTGCTGTTTCTGTTTCGTAAGTCTGTTGAGATATCATATCGTTTGTGTTG 240
 |||||
 Db 195 AACGAGAAGCTGCTGTTTCTGTTTCGTAAGTCTGTTGAGATATCATATCGTTTGTGTTG 254
 |||||
 QY 241 GAGTGTGTGTTCTTTCAAGTCTCTCAAGCTCACTTACTATCATCACTATGACT 300
 |||||
 Db 255 GAGTGTGTGTTCTTTCAAGTCTCTCAAGCTCACTTACTATCATCACTATGACT 314
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 QY 301 CCAGAGAGATATAGAGAGAGTGGATCTTCTGTTTATTAACCTATAGTTGCTCTGCT 360
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 Db 315 CCAGAGAGATATAGAGAGAGTGGATCTTCTGTTTATTAACCTATAGTTGCTCTGCT 374
 |||||
 QY 361 TAGGCTGAGGCTGCTTCTGCTCTGCTAAGAGATGGGCTCGGTCAGCGTCGTAAGGCT 420
 |||||
 Db 375 TAGGCTGAGGCTGCTTCTGCTCTGCTAAGAGATGGGCTCGGTCAGCGTCGTAAGGCT 434
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 QY 421 AACCGTCAAAAAAGAACGCTAAGTCTGAGAGCTCGC 458
 |||||
 Db 435 AACCGTCAAAAAAGAACGCTAAGTCTGAGAGCTCGC 472
 |||||

RESULT 5
 ADR22387
 ID ADR22387 standard; DNA; 472 BP.

AC ADR22387;

DT 07-OCT-2004 (first entry)

XX Agrobacterium tumefaciens plant-optimised Ros selectable marker DNA.

DE repressor-mediated plant selection; transgenic; antibiotic resistance;

KM plant-optimised; Ros selectable marker; ds; gene.

XX Agrobacterium tumefaciens.

OS Synthetic.

XX Key Location/Qualifiers

FT CDS 15..464

FT /product= "Agrobacterium tumefaciens plant-optimised Ros
 FT selectable marker protein"

PN CA2442521-A1.

XX 03-APR-2004.

XX 03-OCT-2003; 2003CA-02442521.

XX 03-OCT-2002; 2002US-0416369P.

XX (MIAC) CANADA MIN AGRICULTURE.

XX Hegedus D, Bate N, Hannoufa A, Lydiat D;

XX WPI; 2004-341154/32.

XX P-PSDB; ADR22389.

PT Repressor-mediated plant selection strategies to identify transgenic
 PT plants comprising using a selectable marker system for plant
 PT transformation that is benign to the plant and confers no advantage to
 PT other organisms after gene transfer.

XX Example 2; SEQ ID NO 1; 125pp; English.

CC The invention relates to novel repressor-mediated plant selection
 CC strategies to identify and select plants, cells, tissue or entire plants
 CC which comprise a coding region of interest. The methods of the invention
 CC may be used for selecting transgenic plants, cells, tissue or entire
 CC plants which comprise a coding region of interest. The methods are not
 CC based on antibiotic resistance, are simple to carry out and provide a
 CC selectable marker system for plant transformation that is benign to the
 CC transformed plant and confers no advantage to other organisms in the
 CC event of gene transfer. The methods involve stringent selection of
 CC transformed cells and use an inexpensive and effective selection agent
 CC that is non-toxic to plant cells. The current sequence is that of the
 CC Agrobacterium tumefaciens plant-optimised Ros selectable marker DNA of
 CC the invention.

CC Sequence 472 BP; 92 A; 110 C; 117 G; 153 T; 0 U; 0 Other;

QY Query Match 100.0%; Score 458; DB 12; Length 472;
 Db Best Local Similarity 100.0%; Pred. No. 2.7e-121;
 Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACTGAGACGCTCTTACGGTAACGCTCAGAGATCTTCTGTTAGCTTACTGCTGATATC 60
 |||||
 Db 15 ATGACTGAGACGCTCTTACGGTAACGCTCAGAGATCTTCTGTTAGCTTACTGCTGATATC 74
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 QY 61 GTTGCTGCTTACGTTTCTAACCAAGTGTTCCTGTTACTAGAGCTTCTGACTTATCTCT 120
 |||||
 Db 75 GTTGCTGCTTACGTTTCTAACCAAGTGTTCCTGTTACTAGAGCTTCTGACTTATCTCT 134
 |||||
 QY 121 GATGTTCAATCTGACATTTCTTGAAACATCTGCTCTGCTTCTGTTGCTTTAAAGTTGAG 180
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 Db 135 GATGTTCAATCTGACATTTCTTGAAACATCTGCTCTGCTTCTGTTGCTTTAAAGTTGAG 194
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 QY 181 AACGAGAAGCTGCTGTTTCTGTTTCGTAAGTCTGTTGAGATATCATATCGTTTGTGTTG 240
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 Db 195 AACGAGAAGCTGCTGTTTCTGTTTCGTAAGTCTGTTGAGATATCATATCGTTTGTGTTG 254
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 QY 241 GAGTGTGTGTTCTTTCAAGTCTCTCAAGCTCACTTACTATCATCACTATGACT 300
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 Db 255 GAGTGTGTGTTCTTTCAAGTCTCTCAAGCTCACTTACTATCATCACTATGACT 314
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 QY 301 CCAGAGAGATATAGAGAGAGTGGATCTTCTGTTTATTAACCTATAGTTGCTCTGCT 360
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 Db 315 CCAGAGAGATATAGAGAGAGTGGATCTTCTGTTTATTAACCTATAGTTGCTCTGCT 374
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 Db 375 TAGGCTGAGGCTGCTTCTGCTCTGCTAAGAGATGGGCTCGGTCAGCGTCGTAAGGCT 434
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 QY 421 AACCGTCAAAAAAGAACGCTAAGTCTGAGAGCTCGC 458
 |||||
 Db 435 AACCGTCAAAAAAGAACGCTAAGTCTGAGAGCTCGC 472
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RESULT 6
 AAD52862
 ID AAD52862 standard; DNA; 447 BP.

XX AAD52862;

XX 14-MAY-2003 (first entry)

XX Agrobacterium tumefaciens ros repressor consensus DNA.

XX ROS repressor protein; gene expression; gene; ds.

XX Agrobacterium tumefaciens.

XX Key Location/Qualifiers

FT CDS 1..447

FT /product= "Ros repressor consensus protein"

FT unsure

FT /tag= b


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Db 181 AARCARBARCCGNGTNGMNGTNGMAAARMSNTNCARAGYGAAYATHTGTTGYYTN 240
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Db 241 GARGYGNGNGMNGTNGMAAARMSNTNCAARCAAYTNACMACNCAYCAVMSNATACN 300
Qy 301 CCAGAGAGATATAGAGAAAGTGGATCTTCTGTTGATTAACCTATGATGCTGCTGCT 360
Db 301 CCNARGARATAYMNGARAAATGGATYTTNCNGTNGATYATYCCNATGCTNGCNCNGCN 360
Qy 361 TAGCGTGAAGCTCGTCTCTGCTGCTTAAGAGATGGGCTCGCTCAAGCTGTAAGCT 420
Db 361 TAYGNGARGCGMNGMNSMNGYTNCGNARARATGGGNTNGNCARMGNGMAARGCN 420
Qy 421 AACCGTCCAAAAAAGAACGCTAAGT 446
Db 421 AAYMNGCCNARARARARMAARGT 446

```

RESULT 7

AD114225 standard; DNA; 447 BP.

AD114225;

22-APR-2004 (first entry)

Plant codon optimised degenerate A_tumefaciens ROS DNA SeqID 3.

ROS; ds; transgenic plant; chromatin remodelling factor;
DNA binding protein; VP16; GAL4; recruitment factor; BnSCL1; BnKCP1;
histone acetyl transferase; HAT; histone deacetylase; HD; HDA; HDAC;
HDA19; cold tolerance.

Agrobacterium tumefaciens.
Synthetic.

MO2003104462-A2.

18-DEC-2003.

06-JUN-2003; 2003WO-CA000822.

06-JUN-2002; 2002US-0387088P.

(MIAC) CANADA DEPT AGRIC & AGRI-FOOD CANADA.

Hannoufa A, Lydiata DJ, Gao M;

WPI; 2004-062364/06.

Regulating expression of a nucleic acid sequence of interest by providing
a eukaryote and growing the eukaryote.

Disclosure; SEQ ID NO 3; 178bp; English.

This invention relates to a novel method for regulating gene expression
in transgenic plants using chromatin remodelling factors. Specifically,
it comprises transforming a plant with one or more constructs comprising
a first nucleotide sequence that is operably linked to a regulatory
region and is capable of binding to a fusion protein, and a second
nucleotide sequence that encodes said fusion protein. This fusion protein
comprises a DNA binding protein (VP16 or GAL4) or a portion thereof,
that can bind to and regulate expression of the gene of interest (i.e.
the first polynucleotide) and a recruitment factor protein (BnSCL1 or
BnKCP1) that can bind to a chromatin remodelling protein. The present
invention describes the chromatin remodelling protein as a histone acetyl
transferase (HAT) or histone deacetylase (referred to as either HD, HDA
or HDAC), which is required to alter the structure of chromatin,
preferably this protein is HDA19. As such, this method can be used to
alter plant characteristics and phenotype e.g. to increase cold tolerance
by regulating the expression of a nucleic acid sequence of interest. This

CC polynucleotide sequence is the degenerate Agrobacterium tumefaciens ROS
CC DNA sequence codon optimised for use in plants, used in an
CC exemplification of the invention.

Sequence 447 BP; 80 A; 53 C; 81 G; 46 T; 0 U; 187 Other;

Query Match 69.2%; Score 317; DB 12; Length 447;

Best local similarity 58.3%; Pred. No. 9e-81;

Matches 260; Conservative 97; Mismatches 89; Indels 0; Gaps 0;

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Qy 1 ATGACTGAGACTGCTTACGCTTAACGCTCAAGATCTTCTGTTAGCTTACTGCTGATATC 60
Db 1 ATGACNGARACNGCNGTNGMAAARMSNTNCAARCAAYTNACMACNCAYCAVMSNATACN 60
Qy 61 GTTGCTGCTTACGCTTCTTCAACGCTTGTTCCTGTTACTGAGCTTCTGGAAGCTTATCT 120
Db 61 GTNGCNGCNTAYGNGMNSNAYCAVGTNGTNCNGTNGARATYTNCCNGGNTNGATHTMSN 120
Qy 121 GATGTTCACTACTGCACTTCTGGAAGATCTGCTGCTTCTGTTGCTTTAAAGTTGAG 180
Db 121 GAYGTCAYACNGCNGTNGMNGTNGMAAARMSNTNCAARCAAYTNACMACNCAYCAVMSNATACN 180
Qy 181 AAGCAGAAAGCTGCTGTTTCTGTTCTGTTAGTCTGTTGAGATGATATCGTTGTTG 240
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Qy 241 GAGTGTGGTGGTCTTTCAAGTCTCTCAAGGCTCACTTACTACTGATGCTGCTGATGACT 300
Db 241 GARTYGNGMNSMNTTAYARMSNTNCAARCAAYTNACMACNCAYCAVMSNATACN 300
Qy 301 CCAGAGAGATATAGAGAAAGTGGATCTTCTGTTGATTAACCTATGATGCTGCTGCT 360
Db 301 CCNARGARATAYMNGARAAATGGATYTTNCNGTNGATYATYCCNATGCTNGCNCNGCN 360
Qy 361 TAGCGTGAAGCTCGTCTCTGCTGCTTAAGAGATGGGCTCGCTCAAGCTGTAAGCT 420
Db 361 TAYGNGARGCGMNGMNSMNGYTNCGNARARATGGGNTNGNCARMGNGMAARGCN 420
Qy 421 AACCGTCCAAAAAAGAACGCTAAGT 446
Db 421 AAYMNGCCNARARARARMAARGT 446

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RESULT 8

AAL56365 standard; DNA; 447 BP.

AAL56365;

22-APR-2004 (first entry)

ROS gene consensus sequence.

Gene expression system; plant; ROS; vector; metabolic engineering; gene;

ds.

Unidentified.

MO2003100063-A1.

04-DEC-2003.

21-NOV-2002; 2002WO-CA001807.

23-MAY-2002; 2002WO-CA000740.

(MIAC) CANADA MIN AGRIC & AGRI-FOOD.

Hannoufa A, Hegeudus D, Bate N;

WPI; 2004-035150/03.

New nucleic acids encoding a ROS repressor optimized for plant codon

PT usage and exhibits ROS operator binding activity, ROS repressor activity
or both, useful for regulating gene expression in plants.

XX Claim 25; Page 93; Opp; English.

XX The present invention relates to a nucleic acid construct comprising a
CC regulatory region operatively linked to a gene of interest and one or
CC more ROS operator sequence capable of controlling the activity of the
CC regulatory region which is functional in plants, encodes a ROS repressor
CC optimised for plant codon usage and exhibits ROS operator binding
CC activity, ROS repressor activity or both. The nucleic acid molecule or
CC its derivative is useful for the regulation of gene expression in plants.
CC The gene expression can be used in metabolic engineering to produce
CC plants that accumulate large amounts of certain intermediate compounds.
CC The present sequence is a polynucleotide used in constructs of the
CC invention

XX Sequence 447 BP; 80 A; 53 C; 81 G; 46 T; 0 U; 187 Other;

XX Query Match 69.2%; Score 317; DB 12; Length 447;

XX Best Local Similarity 58.3%; Pred. No. 9e-81;

XX Matches 260; Conservative 97; Mismatches 89; Indels 0; Gaps 0;

QY 1 ATGACTGAGAGCTGTTACGTTAAGCTCAGAGTCTTCTGTTAGCTTACTGCTGATATC 60
DB 1 ATGACGAGACGCTGTTAAGCTCAGAGTCTTCTGTTAGCTTACTGCTGATATC 60
QY GTTGCTGCTTACGTTTCTTAACCAAGTGTCTCTGTACTGAGCTTCTGAGCTTATCTT 120
DB GTTGCTGCTTACGTTTCTTAACCAAGTGTCTCTGTACTGAGCTTCTGAGCTTATCTT 120
QY 121 GATGTTCAATCTGCACTTTCTGCAACATCTGCTCTCTGCTTCTGTTGTTAACTTGAG 180
DB 121 GATGTTCAATCTGCACTTTCTGCAACATCTGCTCTCTGCTTCTGTTGTTAACTTGAG 180
QY 121 GATGTTCAATCTGCACTTTCTGCAACATCTGCTCTCTGCTTCTGTTGTTAACTTGAG 180
DB 121 GATGTTCAATCTGCACTTTCTGCAACATCTGCTCTCTGCTTCTGTTGTTAACTTGAG 180
QY 181 AAGCAGAAAGCTGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 AAGCAGAAAGCTGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 181 AAGCAGAAAGCTGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 AAGCAGAAAGCTGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 GAGTGTGCTGCTTCTTCAAGTCTCTCAAGCTCCTTACTTACTTACTTACTTACTT 300
DB 241 GAGTGTGCTGCTTCTTCAAGTCTCTCAAGCTCCTTACTTACTTACTTACTTACTT 300
QY 241 GAGTGTGCTGCTTCTTCAAGTCTCTCAAGCTCCTTACTTACTTACTTACTTACTT 300
DB 241 GAGTGTGCTGCTTCTTCAAGTCTCTCAAGCTCCTTACTTACTTACTTACTTACTT 300
QY 301 CCGAGAGATATAGAGAGAGAGTGGATCTTCTGTTGATTAACCTTATGTTGCTCTGCT 360
DB 301 CCGAGAGATATAGAGAGAGAGTGGATCTTCTGTTGATTAACCTTATGTTGCTCTGCT 360
QY 301 CCGAGAGATATAGAGAGAGAGTGGATCTTCTGTTGATTAACCTTATGTTGCTCTGCT 360
DB 301 CCGAGAGATATAGAGAGAGAGTGGATCTTCTGTTGATTAACCTTATGTTGCTCTGCT 360
QY 361 TAGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 361 TAGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 361 TAGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 361 TAGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

QY 421 AACCGTCAAAAAGAGCGTAAGT 446
DB 421 AACCGTCAAAAAGAGCGTAAGT 446

RESULT 9
AAD52860
ID AAD52860 standard; DNA; 429 BP.

XX AAD52860;
XX 14-MAY-2003 (first entry)
XX Agrobacterium tumefaciens ros repressor DNA.
XX Agrobacterium tumefaciens ros repressor protein; gene expression; ds.
XX Agrobacterium tumefaciens.
XX WO200295021-A2.
XX 28-NOV-2002.

XX 23-MAY-2002; 2002MO-CA000740.

XX 23-MAY-2001; 2001US-0292973P.

XX (MIAC) CANADA DEPT AGRIC & AGRI-FOOD CANADA.

XX Hamoufa A, Hegedus D, Bate N;

XX WPI; 2003-148467/14.

XX New nucleic acid molecule encoding a ROS repressor, useful for
PT controlling gene expression in plants, comprises a regulatory region
PT operatively linked to a gene of interest and one or more ROS operator
PT sequence.

XX Example 1; Page 69; 84pp; English.

XX The present invention relates to a novel nucleic acid molecule encoding a
CC ROS repressor protein optimised for plant codon usage and exhibiting ROS
CC operator binding activity and/or ROS repressor activity. The nucleic acid
CC molecule comprises a regulatory region operatively linked to a gene of
CC interest and one or more ROS operator sequence capable of controlling the
CC activity of the regulatory region that is functional in plants. They are
CC useful in controlling gene expression in plants using a repressor protein
CC and corresponding operator sequences. The present sequence is
CC Agrobacterium tumefaciens ros repressor DNA. Note: This sequence is said
CC to encode the repressor protein shown as SEQ ID NO: 21 in page 76 of the
XX specification. However this does not appear to be the case

XX Sequence 429 BP; 94 A; 115 C; 126 G; 94 T; 0 U; 0 Other;

XX Query Match 63.7%; Score 291.6; DB 8; Length 429;

XX Best Local Similarity 80.3%; Pred. No. 1.8e-73;

XX Matches 342; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1 ATGACTGAGAGCTGTTAAGCTCAGAGTCTTCTGTTAGCTTACTGCTGATATC 60
DB 1 ATGACGAGACGCTGTTAAGCTCAGAGTCTTCTGTTAGCTTACTGCTGATATC 60
QY GTTGCTGCTTACGTTTCTTAACCAAGTGTCTCTGTACTGAGCTTCTGAGCTTATCTT 120
DB GTTGCTGCTTACGTTTCTTAACCAAGTGTCTCTGTACTGAGCTTCTGAGCTTATCTT 120
QY GTTGCTGCTTACGTTTCTTAACCAAGTGTCTCTGTACTGAGCTTCTGAGCTTATCTT 120
DB GTTGCTGCTTACGTTTCTTAACCAAGTGTCTCTGTACTGAGCTTCTGAGCTTATCTT 120
QY 121 GATGTTCAATCTGCACTTTCTGCAACATCTGCTCTCTGCTTCTGTTGTTAACTTGAG 180
DB 121 GATGTTCAATCTGCACTTTCTGCAACATCTGCTCTCTGCTTCTGTTGTTAACTTGAG 180
QY 121 GATGTTCAATCTGCACTTTCTGCAACATCTGCTCTCTGCTTCTGTTGTTAACTTGAG 180
DB 121 GATGTTCAATCTGCACTTTCTGCAACATCTGCTCTCTGCTTCTGTTGTTAACTTGAG 180
QY 181 AAGCAGAAAGCTGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 AAGCAGAAAGCTGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 181 AAGCAGAAAGCTGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 AAGCAGAAAGCTGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 GAGTGTGCTGCTTCTTCAAGTCTCTCAAGCTCCTTACTTACTTACTTACTTACTT 300
DB 241 GAGTGTGCTGCTTCTTCAAGTCTCTCAAGCTCCTTACTTACTTACTTACTTACTT 300
QY 241 GAGTGTGCTGCTTCTTCAAGTCTCTCAAGCTCCTTACTTACTTACTTACTTACTT 300
DB 241 GAGTGTGCTGCTTCTTCAAGTCTCTCAAGCTCCTTACTTACTTACTTACTTACTT 300
QY 301 CCGAGAGATATAGAGAGAGAGTGGATCTTCTGTTGATTAACCTTATGTTGCTCTGCT 360
DB 301 CCGAGAGATATAGAGAGAGAGTGGATCTTCTGTTGATTAACCTTATGTTGCTCTGCT 360
QY 301 CCGAGAGATATAGAGAGAGAGTGGATCTTCTGTTGATTAACCTTATGTTGCTCTGCT 360
DB 301 CCGAGAGATATAGAGAGAGAGTGGATCTTCTGTTGATTAACCTTATGTTGCTCTGCT 360
QY 361 TAGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 361 TAGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 361 TAGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 361 TAGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 421 AACCGT 426
DB 421 AACCGT 426

RESULT 10
AAL56363
ID AAL56363 standard; DNA; 429 BP.

```

AC AAL56363;
XX
XX 22-APR-2004 (first entry)
XX
XX A tumefaciens ROS gene.
XX
XX Gene expression system; plant; ROS; vector; metabolic engineering; gene;
XX de.
XX
XX Agrobacterium tumefaciens.
XX
XX W02003100063-A1.
XX
XX 04-DEC-2003.
XX
XX 21-NOV-2002; 2002MO-CA001807.
XX
XX 23-MAY-2002; 2002MO-CA000740.
XX
XX (MIAC ) CANADA MIN AGRIC & AGRI-FOOD.
XX
XX Hannoufa A, Hegedus D, Bate N;
XX
XX WPI; 2004-035150/03.
XX
XX New nucleic acids encoding a ROS repressor optimized for plant codon
XX usage and exhibits ROS operator binding activity, ROS repressor activity
XX or both, useful for regulating gene expression in plants.
XX
XX Disclosure; Page 90-91; Opp; English.
XX
XX The present invention relates to a nucleic acid construct comprising a
XX regulatory region operatively linked to a gene of interest and one or
XX more ROS operator sequence capable of controlling the activity of the
XX regulatory region which is functional in plants, encodes a ROS repressor
XX optimized for plant codon usage and exhibits ROS operator binding
XX activity, ROS repressor activity or both. The nucleic acid molecule or
XX its derivative is useful for the regulation of gene expression in plants.
XX The gene expression can be used in metabolic engineering to produce
XX plants that accumulate large amounts of certain intermediate compounds.
XX The present sequence is a polynucleotide used in constructs of the
XX invention
XX
XX Sequence 429 BP; 94 A; 115 C; 126 G; 94 T; 0 U; 0 Other;
XX
XX Query Match 63.7%; Score 291.6; DB 12; Length 429;
XX Best Local Similarity 80.3%; Pred. No. 1.8e-73;
XX Matches 342; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
XX
XX 1 ATGACTGAGACTGCTTACGCTAAGCTCAGGATCTTCTGTTGAGCTTACTGATATC 60
XX 1 ATGACGGAACCTGATACGCTAAGCTCAGGATCTTCTGTTGAGCTTACTGATATC 60
XX
XX 61 GTTCTGCTTACGCTTCTTACCAAGCTGTTCTGTTACTGAGCTTCTGCACTATCTCT 120
XX 61 GTTCTGCTTACGCTTCTTACCAAGCTGTTCTGTTACTGAGCTTCTGCACTATCTCT 120
XX
XX 61 GTTCTGCTTACGCTTCTTACCAAGCTGTTCTGTTACTGAGCTTCTGCACTATCTCT 120
XX 61 GTTCTGCTTACGCTTCTTACCAAGCTGTTCTGTTACTGAGCTTCTGCACTATCTCT 120
XX
XX 121 GATGTTCACTGACCTTCTGGAACATCTGCTGCTTCTGTTGCTGTTAACTGAG 180
XX 121 GATGTTCACTGACCTTCTGGAACATCTGCTGCTTCTGTTGCTGTTAACTGAG 180
XX
XX 121 GATGTTCACTGACCTTCTGGAACATCTGCTGCTTCTGTTGCTGTTAACTGAG 180
XX 121 GATGTTCACTGACCTTCTGGAACATCTGCTGCTTCTGTTGCTGTTAACTGAG 180
XX
XX 181 AAGCAGAAAGCTGCTGTTCTGTTCTGTTAAGTCTGTTGAGATGATATGTTGTTG 240
XX 181 AAGCAGAAAGCTGCTGTTCTGTTCTGTTAAGTCTGTTGAGATGATATGTTGTTG 240
XX
XX 181 AAGCAGAAAGCTGCTGTTCTGTTCTGTTAAGTCTGTTGAGATGATATGTTGTTG 240
XX 181 AAGCAGAAAGCTGCTGTTCTGTTCTGTTAAGTCTGTTGAGATGATATGTTGTTG 240
XX
XX 241 GAGTGTGCTGTTCTTTCAGATCTCTCAAGGCTCACTTACTACTCTATATGACT 300
XX 241 GAGTGTGCTGTTCTTTCAGATCTCTCAAGGCTCACTTACTACTCTATATGACT 300
XX
XX 241 GAGTGTGCTGTTCTTTCAGATCTCTCAAGGCTCACTTACTACTCTATATGACT 300
XX 241 GAGTGTGCTGTTCTTTCAGATCTCTCAAGGCTCACTTACTACTCTATATGACT 300
XX
XX 301 CCAGAGAGAGTATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
XX 301 CCAGAGAGAGTATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
XX
XX 301 CCAGAGAGAGTATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
XX 301 CCAGAGAGAGTATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360

```

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XX
XX 361 TACCTGAGAGCTGCTTCTGCTCTGCTAAGAGATGGTCTCGCTCAGCTCTAAGCT 420
XX 361 TATGCGGAGAGCCGCTTCTGCGGCTCGCCAGAAATGGTCTCGCTCAGCGCCGCAAGCGC 420
XX
XX 421 AACCGT 426
XX
XX 421 AACCGT 426
XX
XX 421 AACCGT 426
XX
XX
XX
XX RESULT 11
XX ADR22405
XX ID ADR22405 standard; DNA; 429 BP.
XX
XX ADR22405;
XX
XX 07-OCT-2004 (first entry)
XX
XX Agrobacterium tumefaciens wild-type Ros selectable marker DNA.
XX
XX repressor-mediated plant selection; transgenic; antibiotic resistance;
XX wild-type; Ros selectable marker; de; gene.
XX
XX Agrobacterium tumefaciens.
XX
XX Key Location/Qualifiers
XX CDS 1..429
XX FT /product= "Agrobacterium tumefaciens wild-type Ros
XX FT selectable marker protein"
XX
XX CA2442521-A1.
XX
XX 03-APR-2004.
XX
XX 03-OCT-2003; 2003CA-02442521.
XX
XX 03-OCT-2002; 2002US-0416369P.
XX
XX (MIAC ) CANADA MIN AGRICULTURE.
XX
XX Hegedus D, Bate N, Hannoufa A, Lydiat D;
XX
XX WPI; 2004-341154/32.
XX
XX P-PSDB; ADR22407.
XX
XX Repressor-mediated plant selection strategies to identify transgenic
XX plants comprising using a selectable marker system for plant
XX transformation that is benign to the plant and confers no advantage to
XX other organisms after gene transfer.
XX
XX Example 2; SEQ ID NO 19; 125bp; English.
XX
XX The invention relates to novel repressor-mediated plant selection
XX strategies to identify and select plants, cells, tissue or entire plants
XX which comprise a coding region of interest. The methods of the invention
XX may be used for selecting transgenic plants, cells, tissue or entire
XX plants which comprise a coding region of interest. The methods are not
XX based on antibiotic resistance, are simple to carry out and provide a
XX selectable marker system for plant transformation that is benign to the
XX transformed plant and confers no advantage to other organisms in the
XX event of gene transfer. The methods involve stringent selection of
XX transformed cells and use an inexpensive and effective selection agent
XX that is non-toxic to plant cells. The current sequence is that of the
XX Agrobacterium tumefaciens wild-type Ros selectable marker DNA of the
XX invention.
XX
XX Sequence 429 BP; 94 A; 115 C; 126 G; 94 T; 0 U; 0 Other;
XX
XX Query Match 63.7%; Score 291.6; DB 12; Length 429;
XX Best Local Similarity 80.3%; Pred. No. 1.8e-73;
XX Matches 342; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
XX
XX 1 ATGACTGAGACTGCTTACGCTAAGCTCAGGATCTTCTGTTGAGCTTACTGATATC 60

```

```

Db      1 ATAGCGAAACTGCATACGGTAACGCCAGAGATCTGCTGATCGAAGTGAACGGCGGATATT 60
Qy      61 GTTGCTGCTTACGTTTCTTAACCAAGTGTCTCTGTTACTGAGCTTCTGGAATTATCTCT 120
Db      61 GTGGCTGCTATGTTAGCAACCAAGTGTCTCGGTAAGTACTGCCGGCTTATTTTCG 120
Qy      121 GATGTTATCTGACATTTCTGGAACATCTGCTCTCTGCTTCTGTTGTGTTAAAGTTGAG 180
Db      121 GATGTTATCTGACATCTGACATCTGGAACATCTGCTCTCTGCTTCTGTTGTGTTAAAGTTGAG 180
Qy      181 AACGAGAGAGCTGCTGTTTCTGTTCTGTTAAGTCTGTTAGAGATGATCATATCTGTTTGG 240
Db      181 AACGAGAGAGCTGCTGTTTCTGTTCTGTTAAGTCTGTTAAGATGATCATATCTGTTTGG 240
Qy      241 GAGTGTGTTGTTCTTCTTCAAGTCTCTGACGCTGACCTTAATCTATCACTCATGACT 300
Db      241 GAGTGTGTTGTTCTTCTTCAAGTCTCTGACGCTGACCTTAATCTATCACTCATGACT 300
Qy      301 CCGAAGAGATATGAGAGAGAGTGGATCTTCTGTTATTAACCTATGATGTTGCTCTGCT 360
Db      301 CCGAAGAGATATGAGAGAGAGTGGATCTTCTGTTATTAACCTATGATGTTGCTCTGCT 360
Qy      361 TAGCTGAGAGCTGCTTCTGCTCTGCTAAGAGATGAGTCTGCTGACGCTGCTAAGGCT 420
Db      361 TAGCTGAGAGCTGCTTCTGCTCTGCTAAGAGATGAGTCTGCTGACGCTGCTAAGGCT 420
Qy      421 AACCGT 426
Db      421 AACCGT 426

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RESULT 12

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WP AAV30458_1 100001 210000
WP AAV30458_2 200001 310000
WP AAV30458_3 300001 410000
WP AAV30458_4 400001 510000
WP AAV30458_5 500001 534720
ID AAV30458 standard; DNA; 534720 BP.
XX
XX AAV30458;
XX
XX 14-OCT-1998 (first entry)
XX
XX Rhizobium species plasmid pNGR234a.
XX
XX Symbiosis: open reading frame; ORF; plasmid; vector; transportation;
XX degradation; metabolism; host range; nitrogen fixation; nodulation;
XX legume; plant; ds.
XX
XX Rhizobium sp.
XX
XX Key Location/Qualifiers
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XX /product= "oligopeptide permease"
XX /note= "homologous to the OprC gene"
XX 418673..419680
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XX /note= "homologous to the OprD gene"
XX 419677..420738
XX /tag= c
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XX
XX CDS

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FT /product= "encapsulation-like protein"
FT /note= "homologous to the CapA gene"
FT 422628..424031
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FT /product= "aminotransferase-like protein"
FT /note= "homologous to the BioA gene"
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FT /tag= f
FT /standard_name= "ORF K6"
FT /product= "(semi) aldehyde dehydrogenase-like protein"
FT /note= "homologous to the Tmp gene"
FT 428292..429623
FT /tag= g
FT /standard_name= "ORF K7"
FT /product= "transposase homologue"
FT /note= "homologous to the Tnp gene"
FT 429623
FT /tag= h
FT /standard_name= "ORF K8"
FT /product= "glutamate dehydrogenase-like protein"
FT /note= "homologous to the GLUD1 gene"
FT 430538..431284
FT /tag= i
FT /standard_name= "ORF K9"
FT /product= "transposase homologue"
FT /note= "homologous to the Tnp gene"
FT 431284
FT /tag= j
FT /standard_name= "ORF K10"
FT /product= "transposase homologue"
FT /note= "homologous to the Tnp gene"
FT 431284
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FT /standard_name= "ORF K11"
FT /product= "protein of unknown function"
FT /note= "homologous to the FixJ gene"
FT 434107..434433
FT /tag= l
FT /standard_name= "ORF K12"
FT /product= "protein of unknown function"
FT /note= "homologous to the FixJ gene"
FT 434433
FT /tag= m
FT /standard_name= "ORF K13"
FT /product= "ferrodoxin/ferrodoxin-like protein"
FT /note= "homologous to the FdxN gene"
FT 434517..434711
FT /tag= n
FT /standard_name= "ORF K14"
FT /gene= "nifB"
FT /product= "protein involved in FeMo co-factor biosynthesis"
FT /note= "complement (436460..438130)"
FT 436460..438130
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FT /gene= "nifA"
FT /product= "positive regulator of nif, fix and other genes"
FT 438297..438590
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FT function"
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FT /product= "cytochrome P450-like protein"
FT /note= "homologous to the CamC gene"
FT 447844..448500
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FT /product= "gamma-hexachlorocyclohexane-dechlorinase-like
FT protein"
FT /note= "homologous to the LinA gene"
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FT /tag= z
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FT /standard_name= "ORF L4"
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FT /note= "homologous to the LuxA gene"
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FT /tag= ab
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FT /gene= "nifD"
FT /product= "alpha-subunit of FeMo protein of nitrogenase"
FT 454590..456131
FT /tag= ac
FT /standard_name= "ORF L7"
FT /gene= "nifK"
FT /product= "beta-subunit of FeMo protein of nitrogenase"
FT 456187..457677
FT /tag= ad
FT /standard_name= "ORF L8"
FT /product= "protein involved in FeMo co-factor
FT biosynthesis"
FT /note= "homologous to the NifB gene"
FT 457687..459096
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FT /product= "protein involved in FeMo co-factor
FT biosynthesis"
FT /note= "homologous to the FixF gene"
FT 459093..459575
FT /tag= af
FT /standard_name= "ORF L10"
FT /product= "protein of unknown function"
FT /note= "homologous to the NifX gene"
FT 459579..460067
FT /tag= ag
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FT /product= "protein of unknown function"
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FT /product= "protein similar to part of the Fe protein of
FT nitrogenase"
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FT 461228..461545
FT CDS /tag= ai
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FT /product= "protein of unknown function"
FT 463201..464739
FT /tag= aj
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Query Match 43.5%; Score 199.4; DB 2; Length 110000;
Best Local Similarity 67.4%; Pred. No. 4,5e-46;
Matches 281; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

QY 1 ATGACTGAGACTGCTTACCGCTACGCTCAGGATCTTGTGAGCTTACTGCTGATATC 60
DB 16161 ATGACGAAACACAGCTCGGTGCGACGACGACCTTTGGCAGAACTGACGCGAATAATC 16220
QY 61 GTTGCTGCTTACGTTCTTCTAACACAGTTGTTCTGTTACTGAGCTTCTGACTTATCTCT 120
DB 16221 GTAGCCGCCATGTATGACACCCACGATGTTCCGGGTCGAGAGCTTCGACGCTTATCGGCT 16280
QY 121 GATGTTCAATCTGCACTTCTTCTGGAACATGCTGCTGCTTCTTGTGCTTAAAGTTGAG 180
DB 16281 GACGTTCAATTCACCGCTCAACAATGCACTGCTCCGCGCGGTGATTGCTCCCATTTGAG 16340
QY 181 AAGCAGAGCGCTGCTTCTGTTCTGTTGTAAGTCTGTTGAGGATGATATATGTTTGTG 240
DB 16341 AAGCCGAGCGACGCGGTCTGATCCGAAAGTCTGTGCGAGCATGATACATCTGCTTC 16400
QY 241 GAGTGTGTTGTTCTTCTTCAAGTCTCTCAAGCGTCACTTACTGATCATCTATGACT 300
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QY 301 CCAGAGAGTATGAGAGAAAGTGGGATCTTCTGTTGATTAACCTTATGTTGCTCTGCT 360
DB 16461 CCGAAGATTTATGCGAAGATGGGACCTAACCGCGACATACCGGATGTCGCGCCGCT 16520
QY 361 TAGCTGAGGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 417
DB 16521 TAGCGGAAGCCCGCTCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 16577

RESULT 13
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WP Sequence split into 6 fragments
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WP AAV30459_1 100001 210000
WP AAV30459_2 200001 310000
WP AAV30459_3 300001 410000
WP AAV30459_4 400001 510000
WP AAV30459_5 500001 536165
ID AAV30459 standard; DNA; 536165 BP.
XX
AC AAV30459;
XX
DT 06-JUL-1999 (first entry)
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DE Rhizobium species symbiotic plasmid pNGR234.
XX
KW Symbolic; open reading frame; ORF; plasmid; vector; transportation;
XX degradation; metabolism; host range; nitrogen fixation; nodulation;
XX legume; plant; ds.
XX Rhizobium sp.
OS
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Db	19841	CTGTATGGCTAAGTACGCGCTCAAGCCGCAATATCGAAGAAATGGGCTCTCCCGGC	19782
Qy	336	TGATTACCTTATGATTGCTCTGCTTACGCTGAAGCTCGTTCTCTCGCTAAGAGAT	395
Db	19781	TGATTACCCCATGGTGTCTTCAAGCTATGCTCAAAAGCGTTCCGAGCTTGGCGCGCTTT	19722
Qy	396	GGGTCTCGGTCAAGCGCTGTAAGC	419
Db	19721	GGGTCTGGGAAAGAAACGAGCGGC	19698

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 Job time : 488 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 20, 2006, 01:14:38 ; Search time 3647 Seconds
(without alignments)
7022.499 Million cell updates/sec

Title: US-10-719-996A-2

Perfect score: 458
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

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Listing first 45 summaries

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EST.*
1: gb_est1.*
2: gb_est3.*
3: gb_est4.*
4: gb_est5.*
5: gb_est6.*
6: gb_est7.*
7: gb_est8.*
8: gb_est9.*
9: gb_est10.*
10: gb_est11.*
11: gb_gss1.*
12: gb_gss2.*
13: gb_gss3.*
14: gb_gss4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	114	24.9	401	11	AZ577265 07e12 SHO
2	95.6	20.9	257	11	AZ577928 16e11 SHO
3	65.2	14.2	782	11	BH202231 Sml-61C12
4	64	14.0	711	3	BMS588321 170006873
5	63	13.8	581	5	CF569196 EST057 Su
6	63	13.8	774	14	CR237539 Reverse 8
7	63	13.8	969	6	AY383694 Rattus no
8	62.6	13.7	723	11	BH182027 020_K19-
9	62.6	13.7	723	14	CNS07N1N
10	62.4	13.6	1933	6	AY325173 end of
11	62	13.5	475	11	BH209707 Sml-41P23
12	61.6	13.4	1429	10	DT996364 CNB184-A0
13	61	13.3	747	4	CB521826 UI-M-GH0-
14	60.8	13.3	482	11	BH184140 024_U 22-
15	60.8	13.3	482	14	CNS07P5F
16	60.8	13.3	739	11	AZ650033 IM0520C01
17	60.6	13.2	780	5	CF726920 UI-M-HB0-
18	60.6	13.2	818	11	BZ229437 CH230-401
19	60.4	13.2	711	11	BZ098560 CH230-235

20	60	13.1	676	8	CO041542 UI-M-F00-
21	59.6	13.0	479	2	Bj370460
22	59.4	13.0	410	11	BH211305 Sml-50G22
23	59.4	13.0	611	2	BM247568 K0803H04-
24	59.4	13.0	675	4	BY706450
25	59.4	13.0	836	2	B1525376 602924305
26	59.4	13.0	917	4	CB181190 AGENCOURT
27	59.2	12.9	548	11	BH2000391 Sml-39D16
28	58.8	12.8	536	10	DM609105 CGX199-A0
29	58.6	12.8	568	14	DE214279 Trifolium
30	58.6	12.8	906	14	CNS021TL
31	58.4	12.8	477	4	CA743784 Trifolium
32	58.4	12.8	618	14	DE235981
33	58.2	12.7	704	3	BM478868
34	58.2	12.7	710	8	CO543707
35	58.2	12.7	732	11	BZ284533
36	58	12.7	555	2	Bj403974
37	58	12.7	695	2	Bj439038
38	58	12.7	970	14	CNS03H6V
39	57.8	12.6	567	14	FR0006951
40	57.8	12.6	682	10	DM586149
41	57.8	12.6	785	5	CK183608
42	57.8	12.6	790	13	CZ280852
43	57.8	12.6	819	13	CZ285019
44	57.8	12.6	854	4	BX078177
45	57.6	12.6	487	11	BH200321 Sml-50020

ALIGNMENTS

RESULT 1
AZ577265 401 bp DNA linear GSS 08-DEC-2000
LOCUS 07e12 Shot-gun genomic library of Rhizobium strain ANU265
DEFINITION sp. NGR234 genomic clone 07e12, genomic survey sequence.

ACCESSION AZ577265
VERSION AZ577265.1
KEYWORDS GSS.
SOURCE Rhizobium sp. NGR234
ORGANISM Rhizobium sp. NGR234

REFERENCE 1 (bases 1 to 401)
AUTHORS Viprey,V., Rosenthal,A., Broughton,W.J. and Perret,X.
TITLE Genetic snapshots of the Rhizobium species NGR234 genome
JOURNAL Genome Biol. 1 (6), RESEARCH0014 (2000)
PUBMED 11178268

COMMENT Contact: Virginie Viprey
Laboratoire de Biologie Moleculaire des Plantes Superieures
Universite de Geneve
1 Chemin de l'Imperatrice, Chambesey/Geneva 1292, Switzerland
Tel: +44(0)1603450000
Fax: +44(0)1603450045
Email: virginie.viprey@dbsrc.ac.uk
Class: shotgun.

FEATURES
source Location/Qualifiers
1..401
/organism="Rhizobium sp. NGR234"
/mol_type="genomic DNA"
/strain="ANU265"
/db_xref="taxon:394"
/clone="07e12"
/note="Shot-gun genomic library of Rhizobium strain ANU265"

ORIGIN
Query Match 24.9%; Score 114; DB 11; Length 401;
Best Local Similarity 65.8%; Pred. No. 2,4e-21;
Matches 196; Conservative 0; Mismatches 100; Indels 2; Gaps 2;

Qy 1 ATGACTGAGACTGCTTACGGTAACGCTCAGGATCTTGTGTAGCTTACTGCTGATATC 60
 Db 101 ATGAGTAGAATATCGCTTCGGTGCAGACGAATCTCTGTGATGAGCTGACGGCGAATTC 160
 Qy 61 GTTGCTGCTTACGTTTCTAACCAAGTGTTCCTGTTACTGAGCTTCTGACCTTATCTT 120
 Db 161 GTTGCCCGCTACGAGCAACACAGTGTTCCTCGGTCCGACGCTGATATGGCC 220
 Qy 121 GATGTTATCTGACTTTCGGAACATGCTCCTCCTTCTGTGTGTGTTAAGTGTGAG 180
 Db 221 GACCTTATTCGGGCTGCACATATACACGCTCCGCGCGTAGTCGCGGTGAA 280
 Qy 181 AAGCAGAGCCTGC-TGTTCTGTTGCTGTAAGTCTGTTACAGATGATATTCGTTTGT 239
 Db 281 AAGCGAAGCGCGGGGTTTCGTTCCGAAAGTGTGTCAGGACGACAGATCACTTCCCT 340
 Qy 240 GGAATGTGG-TGTTCTTTCAGTCTCTCAAGGCTCACCTTACTACTCATCTCTT 296
 Db 341 CGAATCGCGGGGCTACCTTCMAATGCTGAAGCCCATTTGATGACCCACCAATCT 398

RESULT 2
 A2577928 257 bp DNA linear GSS 08-DEC-2000
 LOCUS 16e11 Shot-gun genomic library of Rhizobium strain ANU265 Rhizobium
 DEFINITION sp. NGR234 genomic clone 16e11, genomic survey sequence.
 ACCESSION A2577928 GI:11604694
 VERSION A2577928.1
 KEYWORDS GSS.
 SOURCE Rhizobium sp. NGR234
 ORGANISM Rhizobium sp. NGR234
 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 Rhizobiaceae; Rhizobium.

REFERENCE 1 (bases 1 to 257)
 Vipey,V., Rosenthal,A., Broughton,W.J. and Perret,X.
 Genetic snapshots of the Rhizobium species NGR234 genome
 Genome Biol. 1 (6), RESEARCH0014 (2000)
 1178268
 CONTACT: Virginie Vipey
 Laboratoire de Biologie Moléculaire des Plantes Supérieures
 University of Geneva
 1 Chemin de l'Imperatrice, Chambesey/Geneva 1292, Switzerland
 Tel: +44(0)1603450000
 Fax: +44(0)1603450045
 Email: virginie.vipey@dbarc.ac.uk
 Class: shotgun;
 Location/Qualifiers

FEATURES
 source
 1..257
 /organism="Rhizobium sp. NGR234"
 /mol_type="genomic DNA"
 /strain="ANU265"
 /db_xref="taxon:394"
 /clone="16e11"
 /clone_lib="Shot-gun genomic library of Rhizobium strain
 ANU265"
 /note="Vector: M13; derivative strain of NGR234 cured of
 pNGR234a"

ORIGIN
 Query Match 20.9%; Score 95.6; DB 11; Length 257;
 Best Local Similarity 67.3%; Pred. No. 4e-16;
 Matches 134; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy 29 AGAATCTTCTTGTGAGCTTACTGCTATATCTGTTGCTGCTTACTTCTTAACACAGCTTG 88
 Db 59 ACGAATCTCTGTGAGCTGACGCGGGAATCGTTGCGCTACGAGCAACACAGCTGG 118
 Qy 89 TTCTGTTACTGAGCTTCTGAGCTTATCTCGATGTTGATGATGACATTTCTGGAACAT 148
 Db 119 TTCCGTTGCGGAGCTGCGACGCTGATGCGGAGCTTCACTTCCGCGCTCAACATACA 178
 Qy 149 CTGCTCTGCTTCTGTTGCTGTTAACGTTGAGAAACAGAACCTGCTGTTTCTGTTGCTA 208

Db 179 CGGCTCCCGCGCGGAGTGTGCTGCGGTGCAAAAGCCGCGGTTTCGTTGCA 238
 Qy 209 AGCTGTTCAAGATGATCA 227
 Db 239 AATGCGTGAAGACAACA 257

RESULT 3
 BH202231/c 782 bp DNA linear GSS 15-NOV-2002
 LOCUS Sml-61C12.TR Sml Schistosoma mansoni genomic clone Sml-61C12,
 DEFINITION genomic survey sequence.
 ACCESSION BH202231
 VERSION BH202231.1 GI:16374489
 KEYWORDS GSS.
 SOURCE Schistosoma mansoni
 ORGANISM Schistosoma mansoni
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigeiida; Schistosomatidae; Schistosomatidae; Schistosoma.
 1 (bases 1 to 782)
 Shetty,J., Simpson,A., Malek,J., Koo,H., Loverde,P.T. and
 El-Sayed,N.M.
 Use of end sequences from Schistosoma mansoni (Puerto Rico strain)
 Sml BAC library for gene discovery and map construction
 Unpublished (2001)
 Other GSS: Sml-61C12.TR
 Contact: Najib M. El-Sayed
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0208
 Fax: 301 838 0208
 Email: nelsayed@tigr.org
 Clones are derived from the Schistosoma mansoni (Puerto Rico) Sml
 BAC library. For clone availability, please contact Dr. Najib
 El-Sayed at TIGR (nelsayed@tigr.org) or Dr. Phillip Loverde at
 State University of New York, Buffalo, New York, USA
 (loverde@buffalo.edu)
 Seq primer: M13 Rev
 Class: BAC ends.
 Location/Qualifiers

FEATURES
 source
 1..782
 /organism="Schistosoma mansoni"
 /mol_type="genomic DNA"
 /strain="Puerto Rico"
 /db_xref="taxon:6183"
 /clone="Sml-61C12"
 /clone_lib="Sml"
 /note="Vector: pBelobAC11; Site 1: Hin dIII; Constructed
 in the laboratory of Dr. Denis Le Paslier at the Fondation
 Jean Dausset, CEPH, Paris, France. Briefly, Schistosoma
 mansoni agarose embedded DNA was partially digested with
 Hin dIII. High molecular weight fragments were ligated in
 pBelobAC11 digested with Hin dIII. The average insert size
 is 100 kb. Total clone coverage: approx. 7.95 X the
 haploid genome. Further information can be found in Le
 Paslier et al. (2000) Construction and characterization of
 a Schistosoma mansoni bacterial artificial chromosome
 library. Genomics 65: 87-94."

ORIGIN
 Query Match 14.2%; Score 65.2; DB 11; Length 782;
 Best Local Similarity 54.1%; Pred. No. 2.7e-07;
 Matches 133; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

Qy 5 CTGAGACTGTTACGTTACGCTCAGAGATCTTGTGTGAGCTTACTGCTGATATCGTTG 64
 Db 405 CTGCTGTTGCTGCTGCTGATGATGATGATGCTGCTGCTGCTGATGATGATG 346
 Qy 65 CTGCTTACGTTTCTAACCAAGTGTTCCTGTACTGAGCTTCTGAGACTTATCTGATG 124
 Db 345 ATGTCGCGGCTGCTTATGATGCTGCTGATGATGATGCTGCTGCTGCTGATGATG 286

QY 125 TTCACTACGACTTTTGTGGAACATCTGCTCCGCTTCTGTGCTGTAAGCTTGAAGC 184
 DB 285 CTGCTGTGTGTAATGCTGCTGTGATGATCTCTGCTGCTGCTGCTGCTGCTG 226
 QY 185 AGAAGCTGCTGTTTCTGTTCTGTAAGCTGTTGAGATGATCATTCGTTTGTGAGT 244
 DB 225 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 166
 QY 245 GTGGTG 250
 DB 165 AAGTTG 160

RESULT 4
 BMS88321 711 bp mRNA linear EST 25-FEB-2002
 LOCUS 17000687322518 A.gam.ad.cdna.blood1 Anopheles gambiae cDNA clone
 DEFINITION 19600449697628 5', mRNA sequence.
 ACCESSION BMS88321 GI:18884182
 VERSION BMS88321.1 GI:18884182
 KEYWORDS EST.
 SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Anopheles gambiae

REFERENCE
 AUTHORS Holt R.A., Lin J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L.,
 Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
 Celera Anopheles gambiae EST project
 COMMENT Unpublished (2002)
 CONTACT: Holt R.A.
 Celera Genomics
 45 W. Gude Dr., Rockville, MD 20850, USA
 Tel: 2404531151
 Fax: 2404534580
 Email: HoltRA@celera.com
 Plate: NU01004AAR row: F column: 14
 Seq primer: M13 Reverse.
 Location/Qualifiers

1. 711
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /strain="RSP-ST (Reduced susc. to Permethrin - std.
 chromosome)"
 /db_xref="taxon:7165"
 /clone="19600449697628"
 /dev_stage="Adult"
 /lab_host="DH10b"
 /clone_1lb="A.Gam.ad.cdna.blood1"
 /note="Vector: pSport1; Site_1: SalI; Site_2: NotI; Whole
 adult mosquitoes (mixed sex) frozen on liquid nitrogen 24
 hours after human blood feeding. cDNA inserts >500 bp
 cloned directionally into pSport 1. Not 1 site is 3'.
 Clones available through the Malaria Research and
 Reference Reagent Resource Center (www.malaria.mr4.org)"

ORIGIN
 Query Match 14.0%; Score 64; DB 3; Length 711;
 Best Local Similarity 48.4%; Pred. No. 5.7e-07;
 Matches 178; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 5 CTGAGACTGCTTACGCTACAGATCTTCTGTTGAGCTTACTGATATCGTTG 64
 DB 643 CTGCTGGGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 584
 QY 65 CTGCTTACGCTTCTTACCAAGCTGTTCTGTTACTAGAGCTTCTGAGACTTATCTGTG 124
 DB 583 CATCTGCTGTGCTGCAATCTGCTGTTGTTGCTGCTGCTGCTGCTGCTGCTG 524
 QY 125 TTCACTACGACTTTTGTGGAACATCTGCTCCGCTTCTGTGCTGTTAAGCTTGAAGC 184
 DB 523 TTGCTGTGTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 464

QY 185 AGAAGCTGCTGTTTCTGTTCTGTAAGCTGTTGAGATGATCATTCGTTTGTGAGT 244
 DB 463 CTGCTGTGTGTAATGCTGCTGTGATGATCTCTGCTGCTGCTGCTGCTGCTG 404
 QY 245 GTGGTGTTCTTCAAGTCTTCAAGCGTCACTTACTATCATCATCTATGACTCCAG 304
 DB 403 TTGCTGTGCTGCTGTTGCTGTTGCTGTTGCTGTTGCTGCTGCTGCTGCTG 344
 QY 305 AGGAGTATAGAGAGAGAGGAGATCTTCTGTTGATTAACCTATGTTGCTCTCTTACG 364
 DB 343 CGGCTGTGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 284
 QY 365 CTGAGCT 372
 DB 283 CTGATGTT 276

RESULT 5
 CF569196 581 bp mRNA linear EST 08-SEP-2004
 LOCUS EST057 Subtracted, Clontech (cat. # K1804-1) Triticum aestivum cDNA
 DEFINITION clone FDC57 5', mRNA sequence.
 ACCESSION CF569196
 VERSION CF569196.1 GI:51921536
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum

REFERENCE
 AUTHORS Xiao, K., Bai, G.H. and Carver, B.F.
 Nylon Filter Arrays Reveal Differential Expression of Expressed
 Sequence Tags in Wheat Roots Under Aluminum Stress
 J. Integr. Plant Biol. 47 (7), 839-848 (2005)
 CONTACT: Guhua Bai
 USDA/ARS and Department of Agronomy
 Kansas State University
 Manhattan, KS 66506, USA
 Email: gbai@bear.agron.ksu.edu
 Seq primer: M13 Forward
 High quality sequence stop: 581.
 Location/Qualifiers

1. 581
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /cultivar="OK91G106"
 /db_xref="taxon:4565"
 /clone="FDC57"
 /issue_type="root"
 /clone_1lb="Subtracted, Clontech (cat. # K1804-1)"
 /note="EST from wheat (Triticum aestivum, cv. OK91G106)
 root in response to aluminum stress"

ORIGIN
 Query Match 13.8%; Score 63; DB 5; Length 581;
 Best Local Similarity 53.4%; Pred. No. 1e-06;
 Matches 132; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 6 TGAGATGCTTACGCTACAGATCTTCTGTTGAGCTTACTGATATCGTTG 65
 DB 324 TGTACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 265
 QY 66 TGTACTGTTTCAACAGCTGTTCTGTTACTAGAGCTTCTGAGACTTATCTGATG 125
 DB 264 TGTACTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 205
 QY 126 TCATCTACGACTTTTGTGGAACATCTGCTCCGCTTCTGTGCTGTTAAGCTTGAAGCA 185
 DB 204 TGTCTGTGTGTTGCTGTTGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTG 145
 QY 186 GAAAGCTGCTGTTTCTGTTCTGTAAGCTCTGTGAGATGATCATATCGTTTGTGAGTG 245

[illegible][illegible]

[illegible]

LOCUS	CNS07071N	723 bp	DNA	linear	GSS 30-NOV-2001
DEFINITION	T3 end of clone 020AF10 of library SmbAC1 from strain Puerto-Rican				
ACCESSION	AL618977				
VERSION	AL618977.1				
KEYWORDS	GSS.				
SOURCE	Schistosoma mansoni				
ORGANISM	Schistosoma mansoni				
REFERENCE	Eukaryotes; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidida; Schistosomatidae; Schistosomatidae; Schistosoma.				
AUTHORS	1 (bases 1 to 723) Le Paslier,M.C., Pierce,R.J., Merlin,F., Hirai,H., Wu,W., Williams,D.L., Johnston,D., Loverde,P.T. and Le Paslier,D.				
TITLE	Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library				
JOURNAL	Genomics 65 (2), 87-94 (2000)				
PUBMED	1078325				
REFERENCE	2 (bases 1 to 723) Genoscope.				
AUTHORS	Direct Submission				
TITLE	Submitted (05-OCT-2001) Genoscope - Centre National de Sequencage :				
JOURNAL	BP 191 91006 EVRY cedex - FRANCE (E-mail : seqr@genoscope.cns.fr				
COMMENT	- Web : www.genoscope.cns.fr) Partially Hind III digested and size-selected S. mansoni cercarial DNA was ligated into Hind III digested pBSIOBAC 11 vector and used to transform E. coli DH10B. The complete library contains 23808 clones from 4 independent sibling-ligation-transformations. Average insert size ranges from 70-127 kb and genome coverage is 7.9-fold.				
FEATURES	Location/Qualifiers 1..723 /organism="Schistosoma mansoni" /mol_type="genomic DNA" /strain="Puerto-Rican" /db_xref="taxon:6183" /clone="020AF10" /clone_lib="SmbAC1" /note="end : T3"				
ORIGIN	Query Match 13.7%; Score 62.6; DB 14; Length 723; Best Local Similarity 53.0%; Pred. No. 1,4e-06; Matches 131; Conservative 1; Mismatches 115; Indels 0; Gaps 0;				
QY	6 TGAGACGCTCTTAACGTAACGCTCAGATCTTCTTGTGAAGCTTACGCTGATATCGTTGC 65				
Db	283 TGATGATGATGATGATGCTCGCGCTGCTTAAATGATGATGATGATCTCGTGTCTAAATGCTGC 224				
QY	66 TGCCTACGTTTCTAACCAAGTGTCTCTGTACTAGAGCTTCCTGAGACTTATCTCTGAGCT 125				
Db	223 TGTGATGATATCTTAAGTCTGCTGTAATGCTGCTGTGATGATATCTCTGCTGTAATGCTGC 164				
QY	126 TCATACGTGCACTTCTGGAACATGTGCTCTCGCTTCTGTTGCTGTTAAAGTTGAGAAGCA 185				
Db	163 TGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 104				
QY	186 GAACCTGCTGCTGTTTCTGTTGTAAGTCTGTTTACAGATGATCAATCGTTTGTGGAGCTG 245				
Db	103 TGA 44				
QY	246 TGGTGGT 252				
Db	43 TGATGAT 37				
RESULT 10	AY325173.c 1933 bp mRNA linear HTC 26-JUL-2003				
LOCUS	AY325173				
DEFINITION	Rattus norvegicus Aa2-050 mRNA, complete cds.				
ACCESSION	AY325173				
VERSION	AY325173.1				
KEYWORDS	Rattus norvegicus (Norway rat)				
SOURCE	HTC.				

[illegible]

RESULT 11	475 bp	DNA	linear	GSS 15-NOV-2002
BH209707/c				
LOCUS				
DEFINITION	Sml-41P23.TF Sml Schistosoma mansoni genomic clone Sml-41P23,			
ACCESSION	BH209707			
VERSION	BH209707			
KEYWORDS	genomic survey sequence.			
ORGANISM	BH209707.1 GI:16388592			
SOURCE	GSS.			
ORGANISM	Schistosoma mansoni			
ORGANISM	Schistosoma mansoni			
ORGANISM	Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;			
ORGANISM	Strigoida; Schistosomatidae; Schistosomatidae; Schistosoma.			
REFERENCE	1 (bases 1 to 475)			
AUTHORS	Shetty,J., Simpson,A., Malek,J., Koo,H., Loverde,P.T. and El-Sayed,N.W.			
TITLE	Use of end sequences from Schistosoma mansoni (Puerto Rico strain) Sml BAC library for gene discovery and map construction			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Najib M. El-Sayed Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: nelsayed@tigr.org Clones are derived from the Schistosoma mansoni (Puerto Rico) Sml BAC library. For clone availability, please contact Dr. Najib El-Sayed at TIGR (nelsayed@tigr.org) or Dr. Phillip Loverde at State University of New York, Buffalo, New York, USA (loverde@buffalo.edu) Seq primer: M13 For Class: BAC ends.			
FEATURES	location/qualifiers			
SOURCE	1..475			
	/organism="Schistosoma mansoni"			
	/mol_type="genomic DNA"			
	/strain="Puerto Rico"			
	/db_xref="taxon:6183"			
	/clone="Sml-41P23"			
	/clone_lib="Sml"			
	/note="Vector: pBelBAC11, Site 1. Hin dIII, Constructed in the laboratory of Dr. Denis Le Paslier at the Fondation Jean Dausset, CEPH, Paris, France. Briefly, Schistosoma mansoni agarose embedded DNA was partially digested with Hin dIII. High molecular weight fragments were ligated in pBelBAC11 digested with Hin dIII. The average insert size is 100 kb. Total clone coverage: approx. 7.95 X the haploid genome. Further information can be found in Le Paslier et al. (2000) Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library. Genomics 65: 87-94."			
ORIGIN				
Query Match	13.5%; Score 62; DB 11; Length 475;			
Best Local Similarity	53.3%; Pred. No. 1,9e-06;			
Matches 131; Conservative	0; Mismatches 115; Indels 0; Gaps 0;			
5	CTGAGACGCTTACGGTACCGTACGATCTTCTGTTGACCTTACTGCTGATATCTGTTG 64			
434	CTGATGCTGCTGCTGCTGATGATGATGATGCTGCTGCTGCTGATGATGATGATGCTG 375			
65	CTGCTTACGTTTCTAACCAAGTTGTTCTGTTACTGAGCTTCTGGAATTATCTTGATG 124			
374	CTGCTGCTGATGCTGCTGTTGATGATCTCTGCTGTTGCTGATGCTGCTGATGATGCTG 315			
125	TTCAATACGACCTTTTCGGAACATCTGCTCTGCTCTGTTGCTGTTAACGTTGGAAGC 184			
314	CTGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGATGATGATGATG 255			
185	AGAAAGCCGCTGTTCTTCTGTTGTAAGCTCTGTTACAGATGATCATATCGTTTGTGAGT 244			

Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Query Match	13.3%	Score 61;	DB 4;	Length 747;
Best Local Similarity	52.6%;	Pred. No. 4.2e-06;		
Matches 133;	Conservative	0;	Mismatches 120;	Indels 0;
			Gaps	0;

Oy	GACGAGACTGGTTACGGTAACGCTCAGGAATCTTGTGTAGACTTACGCGAATAATGCT	62
Db	566 GCGTAGACTGGGCGCTGGGGTTGGGAGAAGACTGCCTGCTGCTGGTGATGGCTGC	507
Oy	63 TGTCTGTACGTTTCTAAACAAGTGTTCCTGTATCAAGTTCCTGGAATTATCTGA	122
Db	506 TGCTGCTCTGTGTGTTGTGTGTGCTGCTGCTGTGTGCTGCTGCTGCTGCTGC	447
Oy	123 TGTTCATCTGCACCTTCTGGAACAATGCTGCTCTGCTGTGTGCTGTAAAGTTGAAA	182
Db	446 TGTGTTCTGTGCTGTGCCGTAAGCAATGCTGCTGCTGCTGTGCTGTGCGATATGTAAC	387
Oy	183 GCAGAGAGCTGCTGTTTCCTGTTCGTAATCTGTTACAGATGATCATATCGTTTGTTTGGA	242
Db	386 TGCTGTGTGTGTGCTGCTGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	327
Oy	243 GTGTGTGTGCTTCT	255
Db	326 TGCTGCTGTGCT	314

RESULT 14	BH184140/c	482 bp	DNA	linear	GSS 19-OCT-2001
LOCUS	BH184140				
DEFINITION	024 J 22-21 SmbAcl1 Schistosoma mansoni genomic clone 024U22 5', genomic survey sequence.				

/note>vector: pBeloBAC 11, Site 1: Hind III; Partially Hind III digested and size-selected S. marcescens DNA was ligated into Hind III digested pBeloBAC 11 vector and used to transform E. coli DH10B. The complete library contains 23808 clones from 4 independent cloning-ligation-transformation. Average insert size ranges from 70-127 kb and genome coverage is 7.9-fold."

ORIGIN

Query Match	13.3%	Score 60.8	DB 11	Length 482
Best Local Similarity	52.8%	Pred. No. 4.2e-06		
Matches 131; Conservative	0	Mismatches 117	Indels 0	Gaps 0

Oy		5	CTGAGACGTGGTAAAGTAACGTCAGAGATCTTTCTTGAGACTTACTGTAATATCGTTG	64
Dd		354	CTAATGCTGAATGCTGCTGCTGCTGCTGCTGATATGATGCTGCCGCCTTATATGATATGATG	295
Oy		65	CTGCTTAAGTTTTAACCAACGTTGTTCCCTGTTACGAGCTTCTGACAATTATCTGTATG	124
Dd		294	ATCTGCTGCTGCTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	235
Oy		125	TTTCACTACGACCTTTTCGAAACATCTGCTCCTGTTCTGCTGCTTAAAGTTGAGAAGC	184
Dd		234	ATCTGCTGCTGCTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGATATGATG	175
Oy		185	AGAAGCCGTGCTGTTCTGTTCTGTTAGTCTGTTACAGATGATCATATCGTTTGGTAGT	244
Dd		174	ATG	115
Oy		245	GTTGCTGGT	252
Dd		114	ATGATGAT	107

RESULT 15				
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LOCUS	CNS07P5F	482 bp	DNA	linear GSS 30-NOV-2000
DEFINITION	T7 end of clone 024DE11 of library SmbAc1 from strain Puerto-Rican of <i>Schistosoma mansoni</i> , genomic survey sequence.			

FEATURES	Location/Qualifiers
source	1. .482

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/organism="Schistosoma mansoni"
/mol_type="genomic DNA"
/strain="Puerto-Rican"
/db_xref="taxon:6183"
/clone="024J22"
/sex="mixed"
/dev_stage="cercariae"
/lab_host="Biomphalaria glabrata"
/clone_lib="SmAC1"

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 22:59:50 ; Search time 161 Seconds
(without alignments)
5322.782 Million cell updates/sec

Title: US-10-719-996A-2

Sequence: 1 atgactgcgactgcgtcgcg.....cgtgaagctcgcgactgcgc 458

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents NA:*

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- 2: /EMC_Celerra_SIDS3/prodata/2/ina/5_COMB.seq:*
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- 9: /EMC_Celerra_SIDS3/prodata/2/ina/RE_COMB.seq:*
- 10: /EMC_Celerra_SIDS3/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	199.4	43.5	536165	3	US-09-214-808-1
2	94.4	20.6	536165	3	US-09-214-808-1
3	68	14.8	486	3	US-09-639-207-13
4	64	14.0	3489	2	US-08-728-323-1
5	64	14.0	3489	3	US-09-298-568-1
6	64	14.0	3489	3	US-09-410-399-1
7	64	14.0	32207	2	US-08-770-379-20
8	64	14.0	32207	3	US-08-757-669A-20
9	64	14.0	32207	3	US-09-230-371A-20
10	64	14.0	32207	3	US-09-481-356C-7
11	58.2	12.7	6558	4	US-09-880-107-1748
12	57.2	12.5	6604	4	US-09-880-107-1748
13	57.2	12.5	6794	3	US-09-491-356C-2
14	54.2	11.8	2718	3	US-09-614-221A-376
15	53.8	11.7	1037	3	US-09-181-585-3
16	53.8	11.7	1159	3	US-09-181-585-3
17	53.8	11.7	1471	3	US-09-181-585-2
18	51.8	11.3	337	3	US-09-253-691-3
19	51.8	11.3	3378	3	US-09-328-352-4107
20	50.6	11.0	203	3	US-09-043-303-7
21	50.4	11.0	7218	2	US-08-232-463-14
22	50.2	11.0	1356	3	US-09-270-767-1416
23	49.6	10.8	8045	5	US-09-913-878A-1

C 24	49.2	10.7	198	7	PCT-US95-10668-1	Sequence 1, Appl1
C 25	49.2	10.7	198	7	PCT-US95-10668-2	Sequence 2, Appl1
C 26	49.2	10.7	629	3	US-09-533-559-943	Sequence 943, App
C 27	48.2	10.5	234	2	US-08-469-802B-3	Sequence 3, Appl1
C 28	48.2	10.5	234	2	US-08-467-803B-3	Sequence 3, Appl1
C 29	47.8	10.4	2183	3	US-10-104-047-1064	Sequence 1064, Ap
C 30	47.6	10.4	198	7	PCT-US95-10668-3	Sequence 3, Appl1
C 31	47.6	10.4	198	7	PCT-US95-10668-4	Sequence 4, Appl1
C 32	47.6	10.4	615	3	US-09-248-796A-3155	Sequence 3155, Ap
C 33	46.6	10.2	477	3	US-09-135-994-1	Sequence 1, Appl1
C 34	46.6	10.2	477	3	US-09-684-843A-1	Sequence 1, Appl1
C 35	46	10.0	533	10	5482709-5	Patent No. 5482709
C 36	46	10.0	533	10	5273901-6	Patent No. 5273901
C 37	45.4	9.9	195	2	US-08-469-802B-2	Sequence 2, Appl1
C 38	45.4	9.9	195	2	US-08-267-803B-2	Sequence 2, Appl1
C 39	45.2	9.9	645	3	US-09-248-796A-12396	Sequence 12396, A
C 40	45	9.8	165	3	US-09-043-303-17	Sequence 17, Appl1
C 41	44.6	9.7	1518	3	US-09-248-796A-5150	Sequence 5150, Ap
C 42	44.6	9.7	3210	3	US-09-270-767-13927	Sequence 13927, A
C 43	44.4	9.7	1740	3	US-09-668-119-1	Sequence 1, Appl1
C 44	44.4	9.7	3334	3	US-09-668-119-2	Sequence 2, Appl1
C 45	44.2	9.7	1129	3	US-10-053-410-1	Sequence 1, Appl1

ALIGNMENTS

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RESULT 1
US-09-214-808-1
Sequence 1, Application US/09214808A
Patent No. 6475793
GENERAL INFORMATION:
APPLICANT: Rosenthal, Andre
APPLICANT: Freiberg, Christoph
APPLICANT: Perret, Xavier Philippe
APPLICANT: Broughton, William John
TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
Patent No. 6475793
FILE REFERENCE: CARP0068
CURRENT APPLICATION NUMBER: US/09/214, 808A
CURRENT FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: PCT/IB97/00950
PRIOR FILING DATE: 1997-07-10
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 536165
TYPE: DNA
ORGANISM: Rhizobium
US-09-214-808-1
Query Match 43.5%; Score 199.4; DB 3; Length 536165;
Best Local Similarity 67.4%; Pred. No. 5.8e-48;
Matches 281; Conservative 0; Mismatches 136; Indels 0; Gaps 0;
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Db 16161 ATGACGAAACCCGCTGCTGCGAGCAACGAACTTTGGCAGAACTGACGCGAATC 16220
QY 61 GTTGCTGCTTACGCTTCTTCAACACGCTGTTCTCTGTTACTGAGCTTCTGACTTACTCT 120
Db 16221 GTAGCGCGCTATGTCAGACCCACGCGGTTCGGGAGCCGAGCTTCGACGCTTATCGCT 16280
QY 121 GATGTCATACGCTGCTTCTGGAACATGCTGCTCTGTTCTGTTCTGTTAAGTTGAG 180
Db 16281 GAGCTTCATTCAGCGCTCAACAATGCACTGCTCCGCCGCGTATGTGCTCCATTGAG 16340
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Db 16341 AAGCCGAAACCGAGCGGTCTGATCCGCAAGTCTGTGACAGATCATCACTCCCTC 16400
QY 241 GAGTGTGTGTGTTCTTTCAGAGTCTCAAGCGTCACTTACTATCATCATCTATGACT 300
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Db 16401 GAATGCGCGCGCGCTTCAAGTGCCTGAGAGCGCACCTTGAATGACCCACCAATCTGTG 16460
Qy 301 CCAAGAGAGATTAAGAGAAAGTGGAGATCTTCTGTATTAATACCTAATAGTTGCTCTGCT 360
Db 16461 CCGGAAAGATTATCGCGAAAGTGGACCTACCGCGGACCTAACCGAATGCTGCGCCGCT 16520
Qy 361 TACGCTAGAGCTCTGCTCTGCTCTGCTAAGAGATGGAGTCTGCTGACGCTGTAAG 417
Db 16521 TATGCGGAAGCCCGCTCGCGTCTGCGCAAGAGATAGCGCTCGCGGACGCGCGGAG 16577

RESULT 2

US-09-214-808-1/c
; Sequence 1, Application US/09214808A
; Patent No. 6475793
; GENERAL INFORMATION:
; APPLICANT: Rosenthal, Andre
; APPLICANT: Freiberg, Christoph
; APPLICANT: Perret, Xavier Philippe
; APPLICANT: Broughton, William John
; TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
; Patent No. 6475793
; TITLE OF INVENTION: Plasmid
; FILE REFERENCE: CARP0068
; CURRENT APPLICATION NUMBER: US/09/214,808A
; CURRENT FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: PCT/IB97/00950
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin Ver. 2.1
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; LENGTH: 536165
; TYPE: DNA
; ORGANISM: Rhizobium
US-09-214-808-1

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Best Local Similarity 54.7%; Pred. No. 9,4e-17;
Matches 210; Conservative 0; Mismatches 171; Indels 3; Gaps 1;

Qy 39 TGTGAGCTTACTGCTGATATGCTGCTGCTTACGTTTCAACACGTTGTTCTGTTAC 98
Db 320081 TCTTGAGCTGACAGCCGCGTGTCTCGGCTTACCTGAGCCGCAATATGTTCTGCGCG 320022
Qy 99 TGAAGCTTCCGAGCTTATCTGTGATGTTCACTGCACTTCTGGAACATCT---GCTCC 155
Db 320021 CGATCTGCGCAGCTTATTCAGCAGAGATCTCTGCTATGACACCTCTCAAGGACGA 319962
Qy 156 TGTCTGTTGCTGTTAAGTTGAGAAAGACAGAACGCTGCTGTTCTGTTCTGTAAGTCTGT 215
Db 319961 CAAAGCTGAGAGAGGCTGCGTGAAGAAACAGCGGCGCGCTCCCGATCAAGAAAGTCACT 319902
Qy 216 TCAGAGATGATATATGTTGTTGAGAGTGTGTGTTCTTCAAGTCTCAAGCTCA 275
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Qy 276 CTTACTACTGATGATGCTATGATCCAGAGAGATTAAGAGAGTGGATCTTCTGCT 335
Db 319841 CTTATGAGCTAAGTACGCGCTCAAGCGCAGCAATATGAGAGAAATGGGCTCTCCGCGC 319782
Qy 336 TGATTAACCTATGTTGCTCTGCTTACGCTAGAGGCTGTTCTGCTCGCTAAGAGAT 395
Db 319781 TGATTAACCTATGTTGCTTCAAGCTATGCTCAAAAGGTTCCGAGCTTGGCGCGCTTT 319722
Qy 396 GGGTCTCGTACGCTGCTAAGC 419
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RESULT 3

US-09-639-207-13/c
; Sequence 13, Application US/09639207

; Patent No. 6815575
; GENERAL INFORMATION:
; APPLICANT: Kazemi-Bafarjani, Parisa
; APPLICANT: Benzer, Seymour
; TITLE OF INVENTION: AN ANIMAL MODEL OF POLYGLUTAMINE
; TITLE OF INVENTION: TOXICITY, METHODS OF USE, AND MODULATORS OF POLYGLUTAMINE
; TITLE OF INVENTION: TOXICITY
; FILE REFERENCE: 06618-686001
; CURRENT APPLICATION NUMBER: US/09/639,207
; CURRENT FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: US 60/148,934
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: US 60/148,933
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: US 60/177,047
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/205,720
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-09-639-207-13

Query Match 14.8%; Score 68; DB 3; Length 486;
Best Local Similarity 48.7%; Pred. No. 2,9e-10;
Matches 185; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

Qy 8 AGACTGCTTACGGTAACGCTCAGATCTTGTGAGCTTACGCTGATATGTTGCTG 67
Db 447 AGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 368
Qy 68 CTTAGCTTTCACACAGCTGTTCTGTTACTGAGCTTCTGCACTTATCTGATGTTTC 127
Db 387 CTGCTGTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 328
Qy 128 ATACTGACTTTCGAAACATCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTG 187
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Qy 188 AGCTGCTGTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 247
Db 267 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 208
Qy 248 GTGATCTTTCACAGCTCTCAAGCTCACTTACTACTATCACTATGAGCTTCAAGAG 307
Db 207 CTGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 148
Qy 308 AGTATAGAGAAAGTGGATCTTCTGTTGATTAACCTATGTTGCTCTGCTTACGCTG 367
Db 147 CTGCTGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 88
Qy 368 AGGCTGTTCTCGTCTGCT 387
Db 87 TTGCTGCTGCTGTTGCTGCT 68

RESULT 4

US-08-728-323A-1/c
; Sequence 1, Application US/08728323A
; Patent No. 5948676
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: Immediate Early Protein From Kaposi's
; TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA

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1  TITLE OF INVENTION: Encoding Same And Uses Thereof
2  NUMBER OF SEQUENCES: 21
3  CORRESPONDENCE ADDRESS:
4  ADDRESSEE: Cooper & Dunham LLP
5  STREET: 1185 Avenue of the Americas
6  CITY: New York
7  STATE: New York
8  COUNTRY: U.S.A.
9  ZIP: 10036
10
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE: Floppy disk
13 COMPUTER: IBM PC compatible
14 OPERATING SYSTEM: PC-DOS/MS-DOS
15 SOFTWARE: PatentIn Release #1.0, Version #1.30
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/08/728,323A
18 FILING DATE:
19 CLASSIFICATION: 435
20 ATTORNEY/AGENT INFORMATION:
21 NAME: White, John P.
22 REGISTRATION NUMBER: 28,678
23 REFERENCE/DOCKET NUMBER: 0575/52268/JPM/MSC/SKS
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: 212-278-0400
26 TELEFAX: 212-391-0525
27 INFORMATION FOR SEQ ID NO. 1:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 3489 base pairs
30 TYPE: nucleic acid
31 STRANDEDNESS: single
32 TOPOLOGY: linear
33 MOLECULE TYPE: DNA (genomic)
34 FEATURE:
35 NAME/KEY: CDS
36 LOCATION: 1..3489
37 US-08-728-323A-1

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Best Local Similarity	46.9%	Pred. No. 1.1e-08		
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Db	2331	CTTAACTCCTGCTCTGCTCTCTCTCTTAATCTCGCTGCTGCTCTCTCTCTCTGCTCTGCTC	2272	
QY	65	CTGCTTACGTTTCTTAAACAGCTGTGTTCTCTGTATCTGAGCTTCCTGGAATCTTATCTGTAGT	124	
Db	2271	CTCTGCTGCTCTCTGTTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2212	
QY	125	TTCATACTGCACTTTCGTGAACATCTGCTCTGCTCTTCTGTGCTGTATTAACGTTGAAGAC	184	
Db	2211	CTGCTGCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2155	
QY	185	AGAAAGCTGCTGTTTCTGTGTGAAGTCTGTTCAGAGATCATATCGTTTGTGTTGAGT	244	
Db	2151	CTCATCTCTGCTGCTCTCTCTCATCTGCTGCTCTGCTGCTCATCTGCTCTCTCTCTGCTCATC	2092	
QY	245	GTGGTGGTCTTCTTCAAGTCTCTCAAGCGCTCACTTACTACTCATCTTATGAATCTCCAG	304	
Db	2091	CTGCTGCTGCTCATCTCTGCTGCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2033	
QY	305	AGAGATATAGAGAGAGAGTGGGATCTTCTGTGTGATTAACCTTAATGGTTGCTCTGTTACG	364	
Db	2031	CTGCTGCTGCTCATCTCTGCTGCTGCTCATCTGCTGCTGCTGCTCATCTCTGCTGCTCATCTC	1972	
QY	365	CTGAGAGCTGTTCTGCTCTGCTGCTAAGAGATGGGCTGCGATCAGCGGTGTGAAGCTTAAC	424	
Db	1971	CTGCTGCTGCTCATCTCTGCTGCTGCTCATCTGCTGCTGCTGCTCATCTCTGCTGCTCATCTC	1912	
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Db	1911	GTGC 1908		

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RESULT 5
US-09-298-568-1/c
: Sequence 1: Application US/09298568
: Patent No. 6322792
: GENERAL INFORMATION:
: APPLICANT: Kleff, Elliott D.
: APPLICANT: Ballestas, Mary E.
: APPLICANT: Kaye, Kenneth M.
: TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
: TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
: FILE REFERENCE: 16412-10001R
: CURRENT APPLICATION NUMBER: US/09/298,568
: CURRENT FILING DATE: 1999-04-21
: EARLIER APPLICATION NUMBER: US 60/109,422
: EARLIER FILING DATE: 1998-11-19
: NUMBER OF SEQ ID NOS: 3
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO: 1
: LENGTH: 3489
: TYPE: DNA
: ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-298-568-1

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Query Match      14.0%; Score 64; DB 3; Length 3489;
Best Local Similarity 46.9%; Pred. No. 1.1e-08;
Matches 199; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

QY      5 CTGAGACTGCTTACGGTAACGCTCAGGATCTCTTCTGTGTGAGCTTACTGCTGATATCGCTG 64
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Db      2331 CTGTAACCTCCGCTCCTGCTGCTCTCTTAACCTCTGCTCCGCTCCTCCTGCTCTGCTC 2272
QY      65 CTGCTTAAGTTTCTTAACCAAGCTGTGTTCTGTACTGAGCTTCCGGAATTATCTGTATG 124
      |||||
Db      2271 CTCTGCTGCTCCTGTTTCACTCATCTGCTGCTGCTCACTCCGCTGCTGCTGCTCATCTG 2211
QY      125 TTCACTACTGCACTTTCGGAACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 184
      |||||
Db      2211 CTGCTGCTGCTCACTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2155
QY      185 AGAAGCCGCTGTTCTTCTGTTGTAAGTCTGTTCAAGATGATCATATCGTTGTTTGAAGT 244
      |||||
Db      2151 CTATCTGCTGCTCCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2097
QY      245 GTGGTGGTTCTTTCAAGTCTCTCAAGGCTCACTTACTACTATCATCTATGACTCCAG 304
      |||||
Db      2091 CTGCTGCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2033
QY      305 AGAGATATAGAGAAAGTGGGATCTTCTGTTGATTAACCTTAATGTTGCTCTGTTACG 364
      |||||
Db      2031 CTGCTGCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTATC 1972
QY      365 CTGAGGCTCGCTTCGCTGCTGCTGAAGGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 424
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Db      1971 CTGCTGCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTATC 1911
QY      425 GTCC 428
      |||
Db      1911 CTGC 1908

RESULT 6
US-09-410-399-1/c
Sequence 1, Application US/09410399
Patent No. 6482587
GENERAL INFORMATION:
APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
FILE REFERENCE: UM-03778
CURRENT APPLICATION NUMBER: US/09/410.399
CURRENT FILING DATE: 1999-10-01

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? NUMBER OF SEQ ID NOS: 6
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 1
? LENGTH: 3489
? TYPE: DNA
? ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-410-399-1

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Query Match	14.0%	Score 64	DB 3	Length 3489
Best Local Similarity	46.9%	Pred. No. 1.1e-08		
Matches 199; Conservative	0	Mismatches 225; Indels	0	Gaps 0

Qy	5	CTGAGACTGCTTAACGGTAAACGCTCAGAGATCTCTGTGAGCTTACTGCTGAATATCGTTG	64
Db	2331	CTTAACTCCGCTGCTGCTGCTCTCTCTAACTCCGCTCCGCTCCTGCTGCTGCTC	2272
Qy	65	CTGCTTACGTTCTTAAACACGTTGTTCTGTATTCTGAGCTTCGTAACCTTATCTGTATG	124
Db	2271	CTCTGCTGCTCCCTGTTTATCTGCTGCTGCTGCTCATCTCGTCTGCTGCTCATCTCTG	2212
Qy	125	TTTCATCTGCACTTCTGTGAACATCTGCTCCGCTCTGTTGCTGTAAAGTTGAAGAC	184
Db	2211	CTGCTGCTGCTCATCTGCTGCTGCTGCTGCTCATCTGCTGCTGCTCATCTGCTGCTG	2155
Qy	185	AGAAAGCTGCTGTTCTGTTCTGTGTAAGTCTGTTCAAGATGATCATATCGTTTGTGAGAT	244
Db	2151	CTCATCTCGCTGCTCTGCTCATCTGCTGCTGCTGCTGCTCATCTGCTGCTGCTCATCT	2092
Qy	245	GTCGTGCTTCTTTCAAGTCTCTCAAGCGTCACTTACTACTATGATGACTCCAG	304
Db	2091	CTGCTGCTGCTCATCTGCTGCTGCTCATCTCGCTGCTGCTCATCTGCTGCTGCTCATCT	2032
Qy	305	AGAGATATAGAGAGAAATGGAGATTTCCGTTGATTACCCATATGTTGCTCTGCTTACG	364
Db	2031	CTGCTGCTGCTCATCTGCTGCTGCTGCTCATCTGCTGCTGCTCATCTGCTGCTGCTCATCT	1972
Qy	365	CTGAGGCTCGTTCTGCTCTGCTGAAGAGATGGATCTCGGTCAGCGTGGTAAGGCTAAC	424
Db	1971	CTGCTGCTGCTCATCTGCTGCTGCTGCTCATCTGCTGCTGCTCATCTGCTGCTGCTCATCT	1912
Qy	425	GTCC 428	
Db	1911	CTGC 1908	

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RESULT 7
US-09-894-273-1/c
; Sequence 1, Application US/09894273
; Patent No. 6756203
; GENERAL INFORMATION:
; APPLICANT: Kieff, Elliott D.
; APPLICANT: Ballestas, Mary E.
; APPLICANT: Kaye, Kenneth M.
; TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
; TITLE OF INVENTION: VIRUS DNA TO MEDICATE EFFICIENT EPISOME PERSISTENCE
; FILE REFERENCE: 16412-10001R
; CURRENT APPLICATION NUMBER: US/09/894,273
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 60/109,422
; PRIOR FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3489
; TYPE: DNA
; ORGANISM: Kapoasi's sarcoma-associated herpesvirus
US-09-894-273-1

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Query Match	14.0%;	Score 64;	DB 3;	Length 3489;
Best Local Similarity	46.9%;	Pred. No. 1.1e-08;		
Matches 199;	Conservative	0;	Mismatches 225;	Indels 0;
			Gaps	0

5 CTGAGACTGCTTACGGTAACGCTCAGGATCTTCTTGTGAGCTTACTGCTGATATCGTTG 64

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Db      2231 CTGTAACCTGCTCCGTCCTGTCCTCTAACTCCTGCTCCTGCTCCCTGCTGCTCTGCTC 2272
Qy      65 CTGCTTAACGTTTCTTAACCAAGTGTTCCTGTTACTAGGCTTCCCTGAGCTTATCTGTGATG 124
Db      2271 CTCTGTGCTGCTCTGTTTCATCCGCTGCTGCTGCTGCTGCTCATCTGCTGCTGCTCATCTCTG 2212
Qy      125 TTCATACTGCACTTTCTGGAACAACCTGCTCCTGCTTCTGTGTGCTGTTAAGTTGAGAAGC 184
Db      2211 CTGCTGTGCTCATCCGCTGCTGCTGCTGCTCATCTGCTGCTGCTGCTGCTCATCCGCTGCTG 2152
Qy      185 AGAAGCTCTGCTTTTCTGTTGCTGAAGTCTGTTCAGATGATCATATGCTTTTGTGAGT 244
Db      2151 CTCATCTGCTGCTCCGCTGCTCATCCGCTGCTCCTGCTGCTCATCCGCTGCTCCTGCTCATC 2092
Qy      245 GTGATGCTTTCTTCAAGTCTCTAAGAGGTCAACCTTAACCTCATCATCTATAGCTCAG 304
Db      2091 CTGCTGCTGCTCATCCGCTGCTGCTGCTCATCTGCTGCTGCTCATCTGCTGCTGCTCATC 2032
Qy      305 AGGAGTATAGAGAAAGTGGATCTTCTGTTGATTAACCTTATGTTGCTCTGCTTACG 364
Db      2031 CTGCTGCTGCTCATCCGCTGCTGCTGCTCATCTGCTGCTGCTCATCCGCTGCTGCTCATC 1972
Qy      365 CTGAGGCTCTTCTTCGCTGCTGCTGAAGATGGTCTCGGCTCAAGCCGTCGAAGCTAAC 424
Db      1971 CTGCTGCTGCTCATCCGCTGCTGCTGCTCATCTGCTGCTGCTCATCCGCTGCTGCTCATC 1912
Qy      425 GTCC 428
Db      1911 CTGC 1908

RESULT 8
US-08-770-379-20
; Sequence 20, Application US/08770379
; Patent No. 5849564
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770.379
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52342
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 3207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

```

```

1      RESULT 8
2      US-08-770-379-20
3      : Sequence 20, Application US/08770379
4      : Patent No. 5849564
5      :
6      : GENERAL INFORMATION:
7      :
8      : APPLICANT: Chang, Yuan
9      : APPLICANT: Bohenzky, Roy A.
10     : APPLICANT: Russo, James J.
11     : APPLICANT: Edelman, Isidore S.
12     : APPLICANT: Moore, Patrick S.
13     :
14     : TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
15     :
16     : TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
17     :
18     : NUMBER OF SEQUENCES: 20
19     :
20     : CORRESPONDENCE ADDRESS:
21     :
22     : ADDRESSEE: Cooper & Dunham LLP
23     :
24     : STREET: 1185 Avenue of the Americas
25     :
26     : CITY: New York
27     :
28     : STATE: New York
29     :
30     : COUNTRY: U.S.A.
31     :
32     : ZIP: 10036
33     :
34     : COMPUTER READABLE FORM:
35     :
36     : MEDIUM TYPE: Floppy disk
37     :
38     : COMPUTER: IBM PC compatible
39     :
40     : OPERATING SYSTEM: PC-DOS/MS-DOS
41     :
42     : SOFTWARE: PatentIn Release #1.0, Version #1.30
43     :
44     : CURRENT APPLICATION DATA:
45     :
46     : APPLICATION NUMBER: US/08/770,379
47     :
48     : FILING DATE:
49     :
50     : CLASSIFICATION: 435
51     :
52     : ATTORNEY/AGENT INFORMATION:
53     :
54     : NAME: White, John P.
55     :
56     : REGISTRATION NUMBER: 28,678
57     :
58     : REFERENCE/DOCKET NUMBER: 52342
59     :
60     : TELECOMMUNICATION INFORMATION:
61     :
62     : TELEPHONE: (212) 278-0400
63     :
64     : TELEFAX: (212) 391-0525
65     :
66     : INFORMATION FOR SEQ ID NO: 20:
67     :
68     : SEQUENCE CHARACTERISTICS:
69     :
70     : LENGTH: 32207 base pairs
71     :
72     : TYPE: nucleic acid
73     :
74     : STRANDEDNESS: double

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US-09-230-371A-20

Query Match 14.0%; Score 64; DB 3; Length 32207;
Best Local Similarity 46.9%; Pred. No. 2.9e-08;
Matches 199; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

QY 5 CTGAGACTGCTTACGTAAGCTGAGATCTTCTTGTGAGCTTACTGCTGATATCTG 64
DB 1966 CTGTAACCTCGCTGCTGCTCTTAACTCTGCTGCTGCTGCTGCTGCTGCTGCTG 19725
QY 65 CTGCTTACGCTTCTTACCAAGCTTGTCTGTACTGAGCTTCCGAGCTATCTCTGATG 124
DB 19726 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 19785
QY 125 TTCACTACGCTTCTGTAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 184
DB 19786 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 19845
QY 185 AGAAGCTGCTGCTTCTGTTGTAAGTCTGTTCAAGATGATCATATGCTTGTGAGAT 244
DB 19846 CTGATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 19905
QY 245 GTGTGCTTCTTCAAGTCTCTCAAGGCTCACTTACTCATCATCTATGATCTCAG 304
DB 19906 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19965
QY 305 AGAGTATAGAGAGAGAGGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 364
DB 19966 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 20025
QY 365 CTGAGGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 424
DB 20026 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 20085
QY 425 GTCC 428
DB 20086 CTGC 20089

RESULT 11

US-09-491-356C-7/C

; Sequence 7, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Gims, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
; FILE REFERENCE: 9465.6US11
; CURRENT APPLICATION NUMBER: US/09/491.356C
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 6558
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-491-356C-7

Query Match 12.7%; Score 58.2; DB 3; Length 6558;
Best Local Similarity 51.8%; Pred. No. 7.6e-07;
Matches 132; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 3 GACTGAGACTGCTTACGTAAGCTGAGATCTTCTTGTGAGCTTACTGCTGATATCTG 62
DB 6380 GCGTGGAGCTGGGGCTGGGGCTGGGGAGAGCTGCTGCTGCTGCTGCTGCTGCTG 6321
QY TGCTGCTTACCTTTTCAACCAAGCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 122

DB 6320 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6261

QY 123 TGCTTACTGCACTTCTGGAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 182
DB 6260 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6201
QY 183 GCAGAACCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 242
DB 6200 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6141
QY 243 GTGTGCTGCTTCTT 257
DB 6140 TGCTGCTGCTGCTGCT 6126

RESULT 12

US-09-880-107-1748/C

; Sequence 1748, Application US/09880107
; Patent No. 6974667
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Schert, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880.107
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1748
; LENGTH: 6604
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. 6974667 D83783
US-09-880-107-1748

Query Match 12.5%; Score 57.2; DB 4; Length 6604;
Best Local Similarity 52.0%; Pred. No. 1.5e-06;
Matches 128; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 3 GACTGAGACTGCTTACGTAAGCTGAGATCTTCTTGTGAGCTTACTGCTGATATCTG 62
DB 6212 GCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6153
QY TGCTGCTTACGCTTCTTAAACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 122
DB 6152 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6093
QY 123 TGCTTACTGCACTTCTGGAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 182
DB 6092 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6033
QY 183 GCAGAACCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 242
DB 6032 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5973
QY 243 GTGTGG 248
DB 5972 GAACGG 5967

RESULT 13

US-09-491-356C-2/C

; Sequence 2, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.


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?   APPLICANT: Gims, Edward I.
?   APPLICANT: Delisi, Lynn
?   TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF X013
?   FILE REFERENCE: 9465.6US11
?   CURRENT APPLICATION NUMBER: US/09/491,356C
?   CURRENT FILING DATE: 2000-01-26
?   PRIOR APPLICATION NUMBER: PCT/US99/09365
?   PRIOR FILING DATE: 1999-04-29
?   PRIOR APPLICATION NUMBER: 60/083,465
?   PRIOR FILING DATE: 1998-04-29
?   NUMBER OF SEQ ID NOS: 24
?   SOFTWARE: PatentIn version 3.1
?   SEQ ID NO 2
?   LENGTH: 6794
?   TYPE: DNA
?   ORGANISM: Homo sapiens
US-09-491-356C-2

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[illegible]

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; RESULT 14
; US-09-614-221A-376/c
; Sequence 376, Application US/09614221A
; Patent No. 6723837
; GENERAL INFORMATION:
; APPLICANT: Karunamanda, Balasulojini
; APPLICANT: Yu, Jaehyuk
; APPLICANT: Kishore, Ganesh M.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
; TITLE OF INVENTION: WITH STEROL SYNTHESIS AND METABOLISM
; FILE REFERENCE: 16516_075
; CURRENT APPLICATION NUMBER: US/09/614,221A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/142,981
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 626
; SEQ ID NO 376
; LENGTH: 2718
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; US-09-614-221A-376

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	Query Match	11.8%;	Score	54.2;	DB	3;	Length	2718;	
	Best Local Similarity	55.6%;	Pred.	No.	7.9e-06;				
	Matches	104;	Conservative	0;	Mismatches	89;	Indels	0; Gaps	0;
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Db	803	TGCTGCTCTGCTGCTGCTGCTGCTGTGTGTATTGTTGCTGTGTGTTGTCGCTGC	744						

[illegible]

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RESULT 15
US-09-181-585-3
; Sequence 3, Application US/09181585
; Patent No. 6524791
; GENERAL INFORMATION:
; APPLICANT: Ranum, Laura P.W.
; APPLICANT: Koob, Michael
; TITLE OF INVENTION: SPINOCEREBELLAR ATAXIA TYPE 8 AND METHODS OF DETECTION
; FILE REFERENCE: 1100900101
; CURRENT APPLICATION NUMBER: US/09/181,585
; CURRENT FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1037
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA
; OTHER INFORMATION: comprising exons E, C, and A
US-09-181-585-3

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[illegible]

Search completed: May 19, 2006, 23:02:42
Job time : 164 secs

Job time : 164 secs

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OM nucleic - nucleic search, using sw model

Run on: May 20, 2006, 01:15:29 ; Search time 1050 Seconds

5359.749 Million cell updates/sec

Title: US-10-719-996A-2

Sequence: 1 atgactgagactgcttacgg.....cgtaaggtctgagagctcgc 458

Scoring table: IDENTITY_NUC

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

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Minimum DB seq length: 0
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1

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA Main:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result	Query	
No.	Score	Match Length DB ID Description

1	458	100.0	458	9	US-10-719-966A-2	Sequence 2, Appl
2	458	100.0	458	10	US-10-995-951A-2	Sequence 2, Appl
3	458	100.0	472	8	US-10-678-490-1	Sequence 1, Appl
4	458	100.0	472	15	US-11-067-425A-3	Sequence 2, Appl
5	317	69.2	447	9	US-10-719-966A-3	Sequence 3, Appl
6	317	69.2	447	10	US-10-995-951A-3	Sequence 3, Appl
7	317	69.2	447	15	US-11-067-425A-3	Sequence 3, Appl
8	291.6	63.7	429	8	US-10-678-490-19	Sequence 19, Appl
9	291.6	63.7	429	9	US-10-719-966A-1	Sequence 1, Appl
10	291.6	63.7	429	10	US-10-995-951A-1	Sequence 1, Appl
11	199.4	20.5	536165	3	US-09-939-964-1	Sequence 1, Appl
12	94.4	43.6	536165	3	US-09-939-964-1	Sequence 1, Appl
13	68	14.8	3486	7	US-10-465-217-13	Sequence 13, Appl
14	64	14.0	3489	3	US-09-894-273-1	Sequence 1, Appl
15	64	14.0	3489	7	US-10-294-804-1	Sequence 1, Appl
16	64	14.0	3489	9	US-10-194-046-1	Sequence 1, Appl
17	60.2	13.1	3660	11	US-10-933-182A-2664	Sequence 2664, Appl

ALIGNMENTS

C 18	59.8	13.1	936	11	US-10-932-182k-166977	Sequence 166977
C 19	59.2	12.9	204803	11	US-10-930-773-325	Sequence 325, App
C 20	57.6	12.6	439	3	US-09-864-761-20174	Sequence 20174, A
C 21	57.4	12.5	3150	3	US-09-938-842k-243	Sequence 243, App
C 22	57.4	12.5	3150	3	US-09-938-842k-243	Sequence 243, App
C 23	57.4	12.5	4283	8	US-10-445-114-4743	Sequence 1474, A
C 24	57.2	12.5	2614	3	US-09-822-846-491	Sequence 491, App
C 25	57.2	12.5	6604	3	US-09-880-107-1748	Sequence 1748, App
C 26	55.2	12.1	3862	13	US-11-097-143-1973	Sequence 1973, App
C 27	55.2	12.1	9614	13	US-11-097-143-1972	Sequence 1972, App
C 28	54.2	11.8	599	16	US-11-136-527-1310	Sequence 1310, App
C 29	54.2	11.8	599	16	US-11-136-527-5406	Sequence 5406, App
C 30	54.2	11.8	2718	9	US-10-793-639-376	Sequence 376, App
C 31	54.2	11.8	3218	8	US-10-451-467k-63	Sequence 63, App
C 32	53.8	11.7	1037	7	US-10-373-667-3	Sequence 3, App
C 33	53.8	11.7	1159	7	US-10-373-667-7	Sequence 1, App
C 34	53.8	11.7	1471	7	US-10-373-667-2	Sequence 2, App
C 35	53.6	11.7	1236	6	US-10-077-584-3	Sequence 3, App
C 36	53	11.6	2742	11	US-10-932-182k-75676	Sequence 75676, A
C 37	52.8	11.5	1400	10	US-10-450-763-189999	Sequence 18999, A
C 38	52.6	11.5	5505	12	US-10-524-823-2	Sequence 2, App
C 39	52.6	11.5	30191	11	US-10-930-773-631	Sequence 631, App
C 40	51.8	11.3	573	7	US-10-029-386-2543	Sequence 2543, App
C 41	51.4	11.2	2731	11	US-10-932-182k-174235	Sequence 174235, A
C 42	50.6	11.0	229	11	US-10-932-182k-174387	Sequence 174387, A
C 43	50.4	11.0	186	11	US-10-932-182k-174145	Sequence 174145, A
C 44	50.4	11.0	2076	13	US-11-097-143-848	Sequence 848, App
C 45	50.4	11.0	2142	11	US-10-932-182k-5700	Sequence 5700, App

RESULT 1

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US-10-719-996A-2
: Sequence 2, Application US/10719996A
: Publication No. US20040224412A1
: GENERAL INFORMATION:
: APPLICANT: Hamouta, Abdelali
: APPLICANT: Hegedua, Dwayne
: APPLICANT: Bate, Nicholas
: TITLE OF INVENTION: A Repressor-Mediated Regulation System for Control of Gene Expression
: TITLE OF INVENTION: in Plants
: FILE REFERENCE: 1096, 021A
: CURRENT APPLICATION NUMBER: US/10/719, 996A
: CURRENT FILING DATE: 2003-11-21
: PRIOR APPLICATION NUMBER: PCT/CA02/00740
: PRIOR FILING DATE: 2002-05-23
: PRIOR APPLICATION NUMBER: US 60/292, 973
: PRIOR FILING DATE: 2001-05-23
: NUMBER OF SEQ ID NOS: 44
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 2
: LENGTH: 458
: TYPE: DNA
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: synthetic ROS optimized for plant codon usage and encoding fusion
: OTHER INFORMATION: of ROS and nuclear localization signal
US-10-719-996A-2

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Query Match	100.0%;	Score 458;	DB 9;	Length 458
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Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACTGAGACTGCTTACCGTAACGCTCAGGATCTTCTTGTGAGCTTACTGCTGATATC 60

Db 1 ATGACTGAGACTGCTTACGGTAACGCTCAGGATCTTCTTGTGAGCTTACTGCTGATATC 60

61 GTTGCTGCTTACGTTTCTAACCAAGTTGTTCCTGTTACTGAGCTTCCCTGGACTTATCTCT 120

Db 61 GTTGCTGCTTACGTTTCTAACCAAGTTGTTCCCTGTTACTGAGCTTCCCTGGACTTATCTCT 120

QY 121 GATGTCATCTGCACTTCTGGAACATCTGCTCTCTCTCTGTTGCTGTTAAAGT 180
DB 121 GATGTCATCTGCACTTCTGGAACATCTGCTCTCTCTCTGTTGCTGTTAAAGT 180
QY 181 AAGCAGAAAGCTGCTGTTCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCT 240
DB 181 AAGCAGAAAGCTGCTGTTCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCT 240
QY 241 GAGTGTGAGTCTTCAAGTCTCAAGGCTCACTTCACTCACTCACTCACT 300
DB 241 GAGTGTGAGTCTTCAAGTCTCAAGGCTCACTTCACTCACTCACTCACT 300
QY 301 CCAAGAGATATAGAGAAAGTGGATCTTCTGTTGATTAACCTATGTTGCTGCT 360
DB 301 CCAAGAGATATAGAGAAAGTGGATCTTCTGTTGATTAACCTATGTTGCTGCT 360
QY 361 TAGCTGAGGCTGCTTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 361 TAGCTGAGGCTGCTTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 421 AACCGTCAAAAAAGAACGCTAAGGCTGAGAGCTGCG 458
DB 421 AACCGTCAAAAAAGAACGCTAAGGCTGAGAGCTGCG 458

RESULT 2

US-10-995-951A-2
Sequence 2, Application US/10995951A
Publication No. US20050245732A1
GENERAL INFORMATION:
APPLICANT: Hamoufa, A. et al.
TITLE OF INVENTION: A Repressor-Mediated Regulation System for Control of Gene Expression
FILE REFERENCE: 1096.021B
CURRENT APPLICATION NUMBER: US/10/995, 951A
CURRENT FILING DATE: 2004-11-23
PRIOR APPLICATION NUMBER: PCT/CA02/01807
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: PCT/CA02/00740
PRIOR FILING DATE: 2002-05-23
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patent version 3.0
SEQ ID NO 2
LENGTH: 458
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic ROS optimized for plant codon usage and encoding fusion
US-10-995-951A-2

Query Match 100.0%; Score 458; DB 10; Length 458;

Best Local Similarity 100.0%; Pred. No. 1e-128; Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACTGAGACTGCTTAACGTAACGCTCAGGATCTTCTGTTGAGTTAGTATGATATC 60
DB 1 ATGACTGAGACTGCTTAACGTAACGCTCAGGATCTTCTGTTGAGTTAGTATGATATC 60
QY 61 GTTGCTGTTACGTTTCTTAACCAAGTGTCTGTTACTGAGCTTCTGAGCTTATCTT 120
DB 61 GTTGCTGTTACGTTTCTTAACCAAGTGTCTGTTACTGAGCTTCTGAGCTTATCTT 120
QY 121 GATGTCATCTGCACTTCTGGAACATCTGCTCTGCTGTTGCTGTTAAAGT 180
DB 121 GATGTCATCTGCACTTCTGGAACATCTGCTCTGCTGTTGCTGTTAAAGT 180
QY 181 AAGCAGAAAGCTGCTGTTCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCT 240
DB 181 AAGCAGAAAGCTGCTGTTCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCT 240
QY 241 GAGTGTGAGTCTTCAAGTCTCAAGGCTCACTTCACTCACTCACTCACT 300
DB 241 GAGTGTGAGTCTTCAAGTCTCAAGGCTCACTTCACTCACTCACTCACT 300

DB 241 GAGTGTGAGTCTTCAAGTCTCAAGGCTCACTTCACTCACTCACTCACT 300
QY 301 CCAAGAGATATAGAGAAAGTGGATCTTCTGTTGATTAACCTATGTTGCTGCT 360
DB 301 CCAAGAGATATAGAGAAAGTGGATCTTCTGTTGATTAACCTATGTTGCTGCT 360
QY 361 TAGCTGAGGCTGCTTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 361 TAGCTGAGGCTGCTTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 421 AACCGTCAAAAAAGAACGCTAAGGCTGAGAGCTGCG 458
DB 421 AACCGTCAAAAAAGAACGCTAAGGCTGAGAGCTGCG 458

RESULT 3

US-10-678-490-1
Sequence 1, Application US/10678490
Publication No. US20040148649A1
GENERAL INFORMATION:
APPLICANT: Lydiate, Derek
APPLICANT: Hamoufa, Abdelali
APPLICANT: Bate, Nicholas
APPLICANT: Hegedus, Dwayne
TITLE OF INVENTION: Repressor Mediated Selection Strategies
FILE REFERENCE: 11089.0003.NPUS01
CURRENT APPLICATION NUMBER: US/10/678,490
CURRENT FILING DATE: 2003-10-03
PRIOR APPLICATION NUMBER: 60/416,369
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patent version 3.1
SEQ ID NO 1
LENGTH: 472
TYPE: DNA
ORGANISM: artificial
FEATURE:
OTHER INFORMATION: Synthetic Ros optimized for plant expression
US-10-678-490-1

Query Match 100.0%; Score 458; DB 8; Length 472;

Best Local Similarity 100.0%; Pred. No. 1e-128; Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACTGAGACTGCTTAACGTAACGCTCAGGATCTTCTGTTGAGTTAGTATGATATC 60
DB 1 ATGACTGAGACTGCTTAACGTAACGCTCAGGATCTTCTGTTGAGTTAGTATGATATC 74
QY 61 GTTGCTGTTACGTTTCTTAACCAAGTGTCTGTTACTGAGCTTCTGAGCTTATCTT 120
DB 61 GTTGCTGTTACGTTTCTTAACCAAGTGTCTGTTACTGAGCTTCTGAGCTTATCTT 134
QY 121 GATGTCATCTGCACTTCTGGAACATCTGCTCTGCTGTTGCTGTTAAAGT 180
DB 121 GATGTCATCTGCACTTCTGGAACATCTGCTCTGCTGTTGCTGTTAAAGT 180
QY 181 AAGCAGAAAGCTGCTGTTCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCT 240
DB 181 AAGCAGAAAGCTGCTGTTCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCT 254
QY 241 GAGTGTGAGTCTTCAAGTCTCAAGGCTCACTTCACTCACTCACTCACT 300
DB 241 GAGTGTGAGTCTTCAAGTCTCAAGGCTCACTTCACTCACTCACTCACT 314
QY 301 CCAAGAGATATAGAGAAAGTGGATCTTCTGTTGATTAACCTATGTTGCTGCT 360
DB 301 CCAAGAGATATAGAGAAAGTGGATCTTCTGTTGATTAACCTATGTTGCTGCT 374
QY 361 TAGCTGAGGCTGCTTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 361 TAGCTGAGGCTGCTTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 434
QY 421 AACCGTCAAAAAAGAACGCTAAGGCTGAGAGCTGCG 458

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Db      435 AACGTCACAAAAAGAAAGCGTAAGCTCTGAGAGCTCCG 472
RESULT 4
US-11-067-425A-2
; Sequence 2, Application US/11067425A
; Publication No. US20050278609A1
; GENERAL INFORMATION:
; APPLICANT: Hannoufa, Abdelali
; APPLICANT: Lydiata, Derek J.
; APPLICANT: Gao, Ming-Jun
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION USING CHROMATIN REMODELLING FACTORS
; FILE REFERENCE: 270.78US11
; CURRENT APPLICATION NUMBER: US/11/067,425A
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US 10/516,753
; PRIOR FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: PCT/CA03/00822
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/387,088
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic ROS
US-11-067-425A-2

Query Match      100.0%; Score 458; DB 15; Length 472;
Best Local Similarity 100.0%; Pred. No. 1e-128;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGACTGAGACTGTTACGGTAACGCTCAGAGATCTTGTGTGAGCTTACGCTGATATC 60
Db      15 ATGACTGAGACTGTTACGGTAACGCTCAGAGATCTTGTGTGAGCTTACGCTGATATC 74
QY      61 GTTGCTGCTTACGTTTCTTAACAACAGTGTTCCTGTTACTAGAGCTTCTGGAATTATCTCT 120
Db      75 GTTGCTGCTTACGTTTCTTAACAACAGTGTTCCTGTTACTAGAGCTTCTGGAATTATCTCT 134
QY      121 GATGTTCACTGACACTTCTTGGAACATCTGCTCTCTCTGTTGCTGTTAAAGTTGAG 180
Db      135 GATGTTCACTGACACTTCTTGGAACATCTGCTCTCTCTGTTGCTGTTAAAGTTGAG 194
QY      181 AAGCAGAGAGCTGCTGTTCTGTTCCGTAAGTCGTGTTGAGATGATCATTCGTTGTTG 240
Db      195 AAGCAGAGAGCTGCTGTTCTGTTCCGTAAGTCGTGTTGAGATGATCATTCGTTGTTG 254
QY      241 GAGTGTGCTGTTCTTCAAGTCTCTCAAGGTCACCTTACTACTCATCTATGACT 300
Db      255 GAGTGTGCTGTTCTTCAAGTCTCTCAAGGTCACCTTACTACTCATCTATGACT 314
QY      301 CCAGAGAGATATAGAGAAAGTGGATCTTCTGTTGATTAACCTATGTTGCTCTGCT 360
Db      315 CCAGAGAGATATAGAGAAAGTGGATCTTCTGTTGATTAACCTATGTTGCTCTGCT 374
QY      361 TAGCTGAGGCTGTTCTGCTCTGCTCAAGAGATGAGTCTCGGTCAGCGCTGTAAGGCT 420
Db      375 TAGCTGAGGCTGTTCTGCTCTGCTCAAGAGATGAGTCTCGGTCAGCGCTGTAAGGCT 434
QY      421 AACCGTCCAAAAAGAAAGCGTAAGCTCTGAGAGCTCCG 458
Db      435 AACCGTCCAAAAAGAAAGCGTAAGCTCTGAGAGCTCCG 472

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RESULT 5
US-10-719-996a-3
; Sequence 3, Application US/10719996A
; Publication No. US2004024412A1

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; GENERAL INFORMATION:
; APPLICANT: Hannoufa, Abdelali
; APPLICANT: Hegedua, Dwayne
; APPLICANT: Bate, Nicholas
; TITLE OF INVENTION: A Repressor-Mediated Regulation System for Control of Gene Express
; FILE REFERENCE: 1096.021A
; CURRENT APPLICATION NUMBER: US/10/719, 996A
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/CA02/00740
; PRIOR FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/292,973
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: ROS consensus sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(447)
; OTHER INFORMATION: n is A or T or G or C
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(447)
; OTHER INFORMATION: h is a or c or t/u
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(447)
; OTHER INFORMATION: m is a or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(447)
; OTHER INFORMATION: r is G or A
; NAME/KEY: misc_feature
; LOCATION: (1)..(447)
; OTHER INFORMATION: y is c/u or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(447)
; OTHER INFORMATION: w is a or t/u
US-10-719-996a-3

Query Match      69.2%; Score 317; DB 9; Length 447;
Best Local Similarity 58.3%; Pred. No. 9.8e-86;
Matches 260; Conservative 97; Mismatches 89; Indels 0; Gaps 0;

QY      1 ATGACTGAGACTGTTACGGTAACGCTCAGAGATCTTGTGTGAGCTTACGCTGATATC 60
Db      1 ATGACNGARACNGCNTATAGGNAAGCNCARGAYTNTGTNGARATNACNGNGAYATH 60
QY      61 GTTGCTGCTTACGTTTCTTAACAACAGTGTTCCTGTTACTAGAGCTTCTGGAATTATCTCT 120
Db      61 GTTGCGCMTATATYATNNSNAAYCAVGTGTCNGCTNACNGARATNACNGNGAYATHWSN 120
QY      121 GATGTTCACTGACACTTCTTGGAACATCTGCTCTGTTGCTGTTAAAGTTGAG 180
Db      121 GATGTCATACNGCNTATNNSNGNACNWSNGCNCNGNNGTNGCNGTNAAYGTNGAR 180
QY      181 AAGCAGAGAGCTGTTCTGTTCCGTAAGTCGTGTTGAGATGATCATATCGTTGTTG 240
Db      181 AACCARAARACNCGNCTNWSNGTNGMNAARWSNGTNCARAGAYCAVATHGTNGYTN 240
QY      241 GAGTGTGCTGTTCTTCAAGTCTCTCAAGGTCACCTTACTACTCATCTATGACT 300
Db      241 GARTGTGNGGNSNTTYAARWSNTYTAARMGNCAYTTNACNCAVCAVWSNATGACN 300
QY      301 CCAGAGAGATATAGAGAAAGTGGATCTTCTGTTGATTAACCTATGTTGCTCTGCT 360

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Db 301 CCNAGARGARTAYMGNAGARATGGGAYTTCNCNGTNGAYTAYCCNATGTCNGCNCNGCN 360
Qy 361 TAGCTGAGGCTGCTCTCGCTAGGAGATGGGTGGCTGAGCGCTGTAAGGCT 420
Db 361 TAGCNGARGCNGMNSMNGNTTNGCNAARGARATGGGNTTNGCARMGNGMAARGCN 420
Qy 421 AACCGTCCAAAAGAAAGCGTAAAGT 446
Db 421 AAYMGNCCNABARABARABARMGNAAAGT 446

RESULT 6
US-10-995-951A-3
; Sequence 3, Application US/10995951A
; Publication No. US20050245732A1
; GENERAL INFORMATION:
; APPLICANT: Hannoufa, A. et al.
; TITLE OF INVENTION: A Repressor-Mediated Regulation System for Control of Gene Expression
; FILE REFERENCE: 1096.021B
; CURRENT FILING DATE: 2004-11-23
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: PCT/CA02/01807
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: PCT/CA02/00740
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Artificial
; OTHER INFORMATION: ROS consensus sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(447)
; OTHER INFORMATION: n is A or T or G or C
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(447)
; OTHER INFORMATION: h is a or c or t/u
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(447)
; OTHER INFORMATION: m is a or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(447)
; OTHER INFORMATION: r is G or A
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(447)
; OTHER INFORMATION: y is t/u or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(447)
; OTHER INFORMATION: w is a or t/u
US-10-995-951A-3

Query Match 69.2%; Score 317; DB 10; Length 447;
Best Local Similarity 58.3%; Pred. No. 9.8e-86;
Matches 260; Conservative 97; Mismatches 89; Indels 0; Gaps 0;

Qy 1 ATGACTGAGCTGCTTACGCTTACGCTTACGCTTCTTTGAGCTTACGCTGATATC 60
Db 1 ATGACNGARACNGCTTACGCTTACGCTTACGCTTCTTTGAGCTTACGCTGATATC 60
Qy 61 GTTGCTGCTTACGCTTACGCTTACGCTTCTTTGAGCTTACGCTTACGCTTACGCT 120
Db 61 GTTGCTGCTTACGCTTACGCTTACGCTTCTTTGAGCTTACGCTTACGCTTACGCT 120
Qy 121 GATGTTCACTGACCTTTCTTGGAACATCTGCTCTGCTTCTGTTGCTTAAAGTTGAG 180

Db 121 GAYTNCAYACNCGNTYTNMSNGNACNMGNGCNCNGCWNMSNGTNGCNGTNAAYTNGAR 180
Qy 181 AACGAGAAGCTGCTTCTTCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCT 240
Db 181 AACGAGAAGCTGCTTCTTCTGCTTACGCTGCTTACGCTGCTTACGCTGCTTACGCT 240
Qy 241 GAGTGTGCTGCTTCTTCAAGCTCTCAAGCGCTACCTTACTATCATCTATGACT 300
Db 241 GAGTGTGCTGCTTCTTCAAGCTCTCAAGCGCTACCTTACTATCATCTATGACT 300
Qy 301 CCNAGAGARTAYMGNAGARATGGGATCTTCTGTTGATTTACCTTATGTTGCTCTGCT 360
Db 301 CCNAGAGARTAYMGNAGARATGGGATCTTCTGTTGATTTACCTTATGTTGCTCTGCT 360
Qy 361 TAGCTGAGGCTGCTCTCGCTAGGAGATGGGTGGCTGAGCGCTGTAAGGCT 420
Db 361 TAGCNGARGCNGMNSMNGNTTNGCNAARGARATGGGNTTNGCARMGNGMAARGCN 420
Qy 421 AACCGTCCAAAAGAAAGCGTAAAGT 446
Db 421 AAYMGNCCNABARABARABARMGNAAAGT 446

RESULT 7
US-11-067-425A-3
; Sequence 3, Application US/11067425A
; Publication No. US20050278809A1
; GENERAL INFORMATION:
; APPLICANT: Hannoufa, Abdelali
; APPLICANT: Lydiate, Derek J.
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION USING CHROMATIN REMODELLING FACTORS
; FILE REFERENCE: 270.78US11
; CURRENT APPLICATION NUMBER: US/11/067,425A
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US 10/516,753
; PRIOR FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: PCT/CA03/00822
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/387,088
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Composite ROS Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(12)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)..(15)
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; NAME/KEY: misc_feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (27)..(27)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (36)..(36)

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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
LOCATION: (111)..(111)
OTHER INFORMATION: n is a, c, g, or t
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NAME/KEY: misc_feature
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LOCATION: (120)..(120)
OTHER INFORMATION: n is a, c, g, or t
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LOCATION: (126)..(126)
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OTHER INFORMATION: n is a, c, g, or t
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LOCATION: (135)..(135)
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NAME/KEY: misc_feature
LOCATION: (138)..(138)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (141)..(141)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (144)..(144)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (147)..(147)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (150)..(150)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (153)..(153)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (156)..(156)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (159)..(159)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (162)..(162)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (165)..(165)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (168)..(168)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (171)..(171)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (177)..(177)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: (192)..(192)
; OTHER INFORMATION: n is a, c, g, or t
;
; FEATURE:
;
; NAME/KEY: misc_feature
; LOCATION: (195)..(195)
; OTHER INFORMATION: n is a, c, g, or t

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Query Match	69.2%	Score 317;	DB 15;	Length 447;
Best Local Similarity	58.3%;	Pred. No. 9.8e-86;		
Matches 260;	Conservative 97;	Mismatches 89;	Indels 0;	Gaps 0;

Qy	1	ATACGAGACCTGCTTAACGCTAACGCTACGAGATCTCTGTGAGCTTACTGCTGATATC	60
Db	1	ATACGAGACCTGCTTAACGCTAACGCTACGAGATCTCTGTGAGCTTACTGCTGATATC	60
Qy	61	GTTCGCTTACGCTTTCTAACCAAGTGTTCCTGTACTGAGCTTCCTGACTATCTCT	120
Db	61	GTTCGCTTACGCTTTCTAACCAAGTGTTCCTGTACTGAGCTTCCTGACTATCTCT	120
Qy	121	GAGTTCATATCTGCACTTCTTGAAACATGTGTCCTGCTTCTGTGGCTGTAAAGCTGAG	180
Db	121	GAGTTCATATCTGCACTTCTTGAAACATGTGTCCTGCTTCTGTGGCTGTAAAGCTGAG	180
Qy	181	AAGCAGAAGCTGCTGCTTTCTGCTGTAAGCTGTTCAGATGATCATATGCTTGTGTTG	240
Db	181	AAGCAGAAGCTGCTGCTTTCTGCTGTAAGCTGTTCAGATGATCATATGCTTGTGTTG	240
Qy	241	GAGTGTGCTGCTTTCTTCAAGTCTCAAGCTGCACTTACTACTCATCTATGACT	300
Db	241	GAGTGTGCTGCTTTCTTCAAGTCTCAAGCTGCACTTACTACTCATCTATGACT	300
Qy	301	CCAGAGAGATATGAGAGAAGTGGAGTCTTCTGTGATTAACCTATGTTGCTCGTCT	360
Db	301	CCAGAGAGATATGAGAGAAGTGGAGTCTTCTGTGATTAACCTATGTTGCTCGTCT	360
Qy	361	TACGCTGAGGCTGTTCCTGCTCGCTAAGAGATGGTCTCGCTCAAGCTCGTAAGCT	420
Db	361	TACGCTGAGGCTGTTCCTGCTCGCTAAGAGATGGTCTCGCTCAAGCTCGTAAGCT	420
Qy	421	AACCGTCCAAAAAAGAACGCTAAAGT	446
Db	421	AATGAGCCAAATAAARAARAAAGT	446

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RESULT 8
US-10-678-490-19
? Sequence 19, Application US/10678490
? Publication No. US20040148649A1
? GENERAL INFORMATION:
? APPLICANT: Lydiatze, Derek
? APPLICANT: Hannoufa, Abdelali
? APPLICANT: Bate, Nicholas
? APPLICANT: Hegedus, Dwayne
? TITLE OF INVENTION: Repressor Mediated Selection Strategies
? FILE REFERENCE: 11089.0003.NUS01
? CURRENT APPLICATION NUMBER: US/10/678.490
? CURRENT FILING DATE: 2003-10-03
? PRIOR APPLICATION NUMBER: 60/416,369
? PRIOR FILING DATE: 2002-10-03
? NUMBER OF SEQ ID NOS: 61
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 19
? LENGTH: 429
? TYPE: DNA
? ORGANISM: Agrobacterium tumefaciens
US-10-678-490-19

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Query Match	63.7%	Score 291.6	DB 8	Length 429
Best Local Similarity	80.3%	Pred. No. 5.3e-78		
Matches 342	Conservative 0	Mismatches 84	Indels 0	Gaps 0
0y	1 ATGACTGAGACGCTTACGGTAACGCTCTTTCTTTGAGCTTACTCGATATAC 60			

Db 1 ATGACGGAAATGCACTACGGTACGCCCAAGATCTGCTGCTGAACCTGACGGCGGATATT 60

QY 61 GTTGCCTGCTTACGTTTCTAACCAAGTGTCTGTACTAGACTTCTGGACTTATCTCT 120

Db 61 GTGGCTGCTTATGTTAGCAACCAAGCTGTTCCGGTAACTGAACTTCCCGCTTATTTGG 120

QY 121 GATGTTACTACTGCACCTTTCTGAAACATCTGTCCTGCTCTGTGCTGTTTAAACCTTGA 180

Db 121 GATGTTCTTACGGCACTCAGCGGAACATCGGCACCGGCATCGGTGGCGGTCAATGTTGAA 180

QY 181 AAGCAGAAGCCGTCGTTTCTGTTCGTAAAGTCTGTTACAGATGATCAATACGTTTGTG 240

Db 181 AAGCAGAAGCCCTGCTGTGTGTTGCGATTCGCAAGTGGTTACAGAGATCATATTCGTCTGTTG 240

QY 241 GAGTGTGTTGTTCTTTCAAGTCTCTCAAGCGCTCACTTACTACTCATCTATAGCT 300

Db 241 GATGTGTTGCTGCTCTTCAAGTCGTCGTAAGCGCCACGCTGACAGCGGATCAACAGATGA 300

QY 301 CCAGAGAGATATAGAGAGAGTGGGATCTTCTGTGTGATTAACCTATAGTTGCTCTGCT 360

Db 301 CCGGAAGAATATCGGAAAAAATGGGATCTGCGCGGTGATTAATCCGATGGTTCTCCCGCC 360

QY 361 TACGCTGAGGCTCTTCTCTGCTCTGCTTAAGAGATGGGCTTGGCTCAAGGTGTGAAGGCT 420

Db 361 TATGCGCAAGCCGTTTCCGCGCTCGCCCAAGAAATGGGCTTGGTCAAGGCGCGCAAGGCG 420

QY 421 AACCGT 426

Db 421 AACCGT 426

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RESULT 9
US-10-719-996A-1
; Sequence 1, Application US/10719996A
; Publication No. US20040224412A1
; GENERAL INFORMATION:
; APPLICANT: Hamnoui, Abdelali
; APPLICANT: Hegedua, Dwayne
; APPLICANT: Bate, Nicholas
; TITLE OF INVENTION: A Repressor-Mediated Regulation System for Control of Gene Expression
; TITLE OF INVENTION: in Plants
; FILE REFERENCE: 1096.021A
; CURRENT APPLICATION NUMBER: US/10/719, 996A
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/CA02/00740
; PRIOR FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/292,973
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-719-996A-1

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Query Match	63.7%	Score 291.6;	DB 9;	Length 429;
Best Local Similarity	80.3%	Pred. No. 5.3e-78;		
Matches 342;	Conservative 0;	Mismatches 84;	Indels 0;	Gaps 0

QY	1	ATGATGAGAC	CTGCTAGCGTACGCTAGAGATCTTCTGTTAGAGCTTACGTGTATATC	60
Db	1	ATGACGGAACTG	CATACGGTACGCCGACGAGATCTGCTGCTGAACTGACGGGGATAT	60
QY	61	GTTCGTGCTTACGTTTCTAACACGCTGTTCTGTCTACGAGCTTCCTGAACTTATCT	120	
Db	61	GTGGCTGCTATGTTAGCAACACGCTGCTCCGGTACCTAGAGCTTCCGGCTTATTTCC	120	
QY	121	GATGTTCACTACGCACTTCTTGAAACATCTGCTCCGCTTCTGTTGCTGTAAAGTTGAG	180	
Db	121	GATGTTCACTACGCACTACGCCGAACATCGGACCCGCACTCGGTGGCGGTCAATGTTGAA	180	


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QY 181 AAGCAGAGGCTGCTGTTCTGTTCTGTAAGTCTGTTCAGAGATGATCATATCTGTTTGG 240
DB 181 AAGCAGAGGCTGCTGTTCTGTTCTGTAAGTCTGTTCAGAGATGATCATATCTGTTTGG 240
QY 241 GAGTGTGAGTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 300
DB 241 GAGTGTGAGTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 300
QY 301 CCAAGAGATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 301 CCAAGAGATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 TAGGCTAGAGCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 420
DB 361 TAGGCTAGAGCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 420
QY 421 AACCGT 426
DB 421 AACCGT 426

RESULT 10
US-10-995-951A-1
; Sequence 1, Application US/10995951A
; Publication No. US20050245732A1
; GENERAL INFORMATION:
; APPLICANT: Hamoufa, A. et al.
; TITLE OF INVENTION: A Repressor-Mediated Regulation System for Control of Gene Express
; FILE REFERENCE: 1096.021B
; CURRENT APPLICATION NUMBER: US/10/995,951A
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: PCT/CA02/01807
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: PCT/CA02/00740
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patent version 3.0
; SEQ ID NO 1
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-995-951A-1

Query Match 63.7%; Score 291.6; DB 10; Length 429;
Best Local Similarity 80.3%; Pred. No. 5.3e-78;
Matches 342; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1 ATGACTGAGACTGCTTACCGTAAAGCTCAGATCTTCTGTTGAGCTTACTGCTGATATC 60
DB 1 ATGACGAGAACTGATACGATACGTAAGCCAGATCTGCTGTCGAACTGACGCGGATATT 60
QY 61 GTTCTGCTTACGTTTCTTAAACAGGTTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 120
DB 61 GTTCTGCTTACGTTTCTTAAACAGGTTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 120
QY 121 GATGTTCACTGATCTTCTGTAACATCTGCTCTGCTCTGTTCTGTTCTGTTCTGTTCTG 180
DB 121 GATGTTCACTGATCTTCTGTAACATCTGCTCTGCTCTGTTCTGTTCTGTTCTGTTCTG 180
QY 181 AAGCAGAGGCTGCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 240
DB 181 AAGCAGAGGCTGCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 240
QY 241 GAGTGTGAGTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 300
DB 241 GAGTGTGAGTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 300
QY 301 CCAAGAGATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 301 CCAAGAGATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 TAGGCTAGAGCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 420
DB 361 TAGGCTAGAGCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 420
```

```
DB 361 TAGGCTAGAGCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 420
QY 421 AACCGT 426
DB 421 AACCGT 426

RESULT 11
US-09-939-964-1
; Sequence 1, Application US/09939964
; Publication No. US20030054522A1
; GENERAL INFORMATION:
; APPLICANT: Rosenthal, Andre
; APPLICANT: Freiberg, Christoph
; APPLICANT: Perret, Xavier Philippe
; APPLICANT: Broughton, William John
; TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
; FILE REFERENCE: CARP0068
; CURRENT APPLICATION NUMBER: US/09/939,964
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/214,808
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 1
; LENGTH: 536165
; TYPE: DNA
; ORGANISM: Rhizobium
US-09-939-964-1

Query Match 43.5%; Score 199.4; DB 3; Length 536165;
Best Local Similarity 67.4%; Pred. No. 2.6e-48;
Matches 281; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

QY 1 ATGACTGAGACTGCTTACCGTAAAGCTCAGATCTTCTGTTGAGCTTACTGCTGATATC 60
DB 16161 ATGACAGAAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 16220
QY 61 GTTCTGCTTACGTTTCTTAAACAGGTTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 120
DB 16221 GTAGCCGCTATATGACAGACCCAGCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 16280
QY 121 GATGTTCACTGATCTTCTGTAACATCTGCTCTGCTCTGTTCTGTTCTGTTCTGTTCTG 180
DB 16281 GAGTTCATTCAGCGCTCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 16340
QY 181 AAGCAGAGGCTGCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 240
DB 16341 AACCCAGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 16400
QY 241 GAGTGTGAGTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 300
DB 16401 GAATGCGGCGGCGCTTCAAGTGTGCTGAGACGCACTGATGACCAACATCTGCTG 16460
QY 301 CCAAGAGATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 16461 CCGAGAGATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 16520
QY 361 TAGGCTAGAGCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 420
DB 16521 TAGGCTAGAGCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 420

RESULT 12
US-09-939-964-1/c
; Sequence 1, Application US/09939964
; Publication No. US20030054522A1
; GENERAL INFORMATION:
; APPLICANT: Rosenthal, Andre
; APPLICANT: Freiberg, Christoph
; APPLICANT: Perret, Xavier Philippe
```

APPLICANT: Broughton, William John
TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
FILE REFERENCE: CARP0068
CURRENT APPLICATION NUMBER: US/09/939,964
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 09/214,808
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 536165
TYPE: DNA
ORGANISM: Rhizobium
US-09-939-964-1

Query Match 20.6%; Score 94.4; DB 3; Length 536165;
Best Local Similarity 54.7%; Pred. No. 2.7e-16;
Matches 210; Conservative 0; Mismatches 171; Indels 3; Gaps 1;

39 TGTGAGCTTACTGCTGATATCGTTGCTGCTTACGTTTCAACGCGTTGCTGTTAC 98
320081 TCTTGAGCTGACAGCCGGGTTGCTGCGCTTACTGAGCCGCAATTCGTTCTGCCGC 320022
99 TGAGCTTCTGAGCTTATCTCTGATGTTCAATGCACTTCTGGAACATCT--GCTCC 155
320021 CGATCTGCCAGCTTATATGACAGAGATCTCTGCTATGACAGCACTTCAAGGAGA 319962
156 TGCTTCCTGCTGTTTAACTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 215
319961 CAAAGCTGAG 319902
216 TCAGAGATGATATCGTTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 275
319901 GAGCGAGAGCTTATCATATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 319842
276 CCTTACTACTCATCATCTATGATCTCAAGAGAGATGAGAGAGAGAGAGAGAGAG 335
319841 CCTGATGCTTAAAGTACGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 319782
336 TGATTACCTATGCTGCTGCTGCTTACGCTGAGAGAGAGAGAGAGAGAGAGAGAG 395
319781 TGATTACCTATGCTGCTGCTTACGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 319722
396 GAGTCTCGTACGCTGTAAGC 419
319721 GGGTCTGGAGAAAGAGAGAGAGC 319698

RESULT 13
US-10-465-217-13/c
Sequence 13, Application US/10465217
Publication No. US20030204859A1
GENERAL INFORMATION:
APPLICANT: Kazemi-Bafarjani, Parisa
APPLICANT: Benzer, Seymour
TITLE OF INVENTION: AN ANIMAL MODEL OF POLYGLUTAMINE
TITLE OF INVENTION: TOXICITY, METHODS OF USE, AND MODULATORS OF POLYGLUTAMINE
FILE REFERENCE: 06618-685001
CURRENT APPLICATION NUMBER: US/10/465,217
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: US/09/639,207
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: US 60/148,934
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: US 60/148,933
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: US 60/177,047
PRIOR FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 60/205,720
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 69

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 486
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic DNA
US-10-465-217-13

Query Match 14.8%; Score 68; DB 7; Length 486;
Best Local Similarity 48.7%; Pred. No. 8.4e-10;
Matches 185; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

8 AGAGCTTACAGCTTAAAGCTCAGAGATCTTCTGTTGAGCTTAACTGCTGATATGCTG 67
447 AGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 368
68 CTTAAGTTTCTAACACAGCTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTT 127
387 CTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 328
128 ATACGCACTTCTGGAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 187
327 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 268
188 AGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 247
267 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 208
248 GGTGCTTCTTCAAGCTTCTCAAGCTTCTCAAGCTTCTCAAGCTTCTCAAGCTTCTCA 307
207 CTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 148
308 AGTATGAG 367
147 CTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 88
368 AGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 387
87 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 68

RESULT 14
US-09-894-273-1/c
Sequence 1, Application US/09894273
Publication No. US20040037847A1
GENERAL INFORMATION:
APPLICANT: Kiehl, Elliott D.
APPLICANT: Ballester, Mary E.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
FILE REFERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/894,273
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/109,422
PRIOR FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 3489
TYPE: DNA
ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-894-273-1

Query Match 14.0%; Score 64; DB 3; Length 3489;
Best Local Similarity 46.9%; Pred. No. 3.8e-08;
Matches 199; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

5 CTGAGACTGCTTACGAGTACGAGATCTTCTGTTGAGCTTACGCTGATATGCTG 64
2331 CTCTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2272

QY 65 CTGCTTACGTTTTCACGAGTTTTCGTGTAATGAGCTTCTGAGACTTATCTGATG 124
|||
Db 2271 CTCTGCTGCTCCGTTTCATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2212
|||
QY 125 TTCAATACGACCTTTTGAACAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 184
|||
Db 2211 CTGCTGCTGCTCATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2152
|||
QY 185 AGAAGCTGCTGTTTCTGTTGTAAGTCTGTTAGATGATGATGATGATGATGATGATGATG 244
|||
Db 2151 CTGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2092
|||
QY 245 GTGCTGTTTTCATCAAGTCTCTCAAGGCTGACCTTACTCATCATCATCATCATCATCAT 304
|||
Db 2091 CTGCTGCTGCTCATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2032
|||
QY 305 AGAGATATAGAGAGAGAGAGAGATCTCTGTTGATTAACCTATGATGATGATGATGATG 364
|||
Db 2031 CTGCTGCTGCTCATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1972
|||
QY 365 CTGAGGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 424
|||
Db 1971 CTGCTGCTGCTCATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1912
|||
QY 425 GTCC 428
|||
Db 1911 CTGC 1908
|||

RESULT 15

US-10-294-804-1/c
; Sequence 1, Application US/10294804
; Publication No. US2003013948A1
; GENERAL INFORMATION:
; APPLICANT: Robertson, Erle S.
; APPLICANT: Collier, Murray A.
; TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
; FILE REFERENCE: UM-03778
; CURRENT APPLICATION NUMBER: US/10/294,804
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US/09/410,399
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3489
; TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-10-294-804-1

Query Match 14.0%; Score 64; DB 7; Length 3489;
Best Local Similarity 46.9%; Pred. No. 3.8e-08;
Matches 199; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

QY 5 CTGAGACTGCTTACGCTGACGCTCAGAGATCTTCTGTTGAGCTTACTGCTGATATCGTTG 64
|||
Db 2231 CTCTAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2272
|||
QY 65 CTGCTTAAGTTTTCACAGGTTTCTGTTACTGAGCTTCCGGAATATCTGATG 124
|||
Db 2271 CTCTGCTGCTCCGTTTCATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2212
|||
QY 125 TTCAATACGACCTTTTGAACAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 184
|||
Db 2211 CTGCTGCTGCTCATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2152
|||
QY 185 AGAAGCTGCTGTTTCTGTTGTAAGTCTGTTAGATGATGATGATGATGATGATGATGATG 244
|||
Db 2151 CTGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2092
|||
QY 245 GTGCTGTTTTCATCAAGTCTCTCAAGGCTGACCTTACTCATCATCATCATCATCATCAT 304
|||

Db 2091 CTGCTGCTGCTCATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2032
|||
QY 305 AGAGATATAGAGAGAGAGAGATCTCTGTTGATTAACCTATGATGATGATGATGATG 364
|||
Db 2031 CTGCTGCTGCTCATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1972
|||
QY 365 CTGAGGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 424
|||
Db 1971 CTGCTGCTGCTCATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1912
|||
QY 425 GTCC 428
|||
Db 1911 CTGC 1908
|||

Search completed: May 20, 2006, 01:45:40
Job time : 1052 secs

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

- Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
- Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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```

; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174387
; LENGTH: 279
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-174387
```

```

Query Match      11.0%; Score 50.6; DB 7; Length 279;
Best Local Similarity 51.0%; Pred. No. 5.7e-07;
Matches 116; Conservative 0; Mismatches 109; Indels 0; Gaps 0;
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QY 33 TCTTCTGTGAGCTTACTGCTGATATCGTTCGCTTACGTTTCTAACACAGTTGTC 92
DB 250 TGTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 191
QY 93 TGTACTGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 152
DB 190 TGTGTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 131
QY 153 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 212
DB 130 TGTGTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 71
QY 213 TGTTCAGATGATCATATCGTTGTTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 257
DB 70 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 26
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RESULT 6
US-11-217-529-174145/C
; Sequence 174145, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174145
; LENGTH: 186
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-174145
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```

Query Match      11.0%; Score 50.4; DB 7; Length 186;
Best Local Similarity 55.0%; Pred. No. 5.4e-07;
Matches 99; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
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QY 25 GCTCAGATCTTCTGTTGAGCTTACTGCTGATATCGTTCGCTTACGTTTCTAACAC 84
DB 186 GCTGTGTGTGTGCTGTAAGCCTGCAACTGATGCTGTGTGTGTGTGTGTGTGTGTGT 127
```

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QY 85 GTTGTTCCTGTTACTGAGCTTCCTGAGCTTATCTGATCTGATGTTCACTGCACTTTCGA 144
DB 126 GTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 67
QY 145 ACATCTGCTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 204
DB 66 GCTGCTGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7
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RESULT 7
US-11-217-529-5700/C
; Sequence 5700, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5700
; LENGTH: 2142
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5700
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```

Query Match      11.0%; Score 50.4; DB 7; Length 2142;
Best Local Similarity 55.0%; Pred. No. 1.8e-06;
Matches 99; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
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```

QY 25 GCTCAGATCTTCTGTTGAGCTTACTGCTGATATCGTTCGCTTACGTTTCTAACAC 84
DB 1168 GCTGTGTGTGTGCTGTAAGCCTGCAACTGATGCTGTGTGTGTGTGTGTGTGTGTGT 1109
QY 85 GTTGTTCCTGTTACTGAGCTTCCTGAGCTTATCTGATGTTCACTGCACTTTCGA 144
DB 1108 GTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1049
QY 145 ACATCTGCTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 204
DB 1048 GCTGCTGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 989
```

```

RESULT 8
US-11-217-529-2946/C
; Sequence 2946, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2946
; LENGTH: 2151
; TYPE: DNA
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ORGANISM: Saccharomyces pastorianus
US-11-217-529-2946

Query Match 10.8%; Score 49.4; DB 7; Length 2151;
Best Local Similarity 54.7%; Pred. No. 3.7e-06;
Matches 98; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 50 CTGCTGATATCGTGTGCTTACGTTCTTAACCAAGTGTCCGCTTACTAGAGCTTCCTG 109
DB 1767 CTCTGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 1708
QY 110 GACTTATCTGTGATGTTCAATGCACTTCTGGAACATGCTCCTGCTTGTGCTG 169
DB 1707 TTGTTGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1648
QY 170 TTAACGTTGGAAGCAAGCAAGCTGCTGCTTCTGTGCTAGTCTGTTCAGAGATGATAT 228
DB 1647 CTGCTGTGTGCTGTAATTTGCTGCTGTGCTGCACTTGTGTGACCATATTCGCAT 1589

RESULT 9
US-11-217-529-2150/c
Sequence 2150, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: KODAMA, NORIHISA
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIRO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217, 529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 2150
LENGTH: 2304
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-2150

Query Match 10.4%; Score 47.6; DB 7; Length 2304;
Best Local Similarity 50.9%; Pred. No. 1.3e-05;
Matches 113; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 12 TGCTTAAGCTAAGCTCAGATCTTCTTGAAGCTTACTGCTGATATCGTGTGCTGCTTA 71
DB 761 TGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 702
QY 72 CGTTTCAACCAAGTGTGCTGCTTACTGAGCTTCTGGAATATCTTCTGATGTTCAATAC 131
DB 701 TGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 642
QY 132 TGCACTTCTGGAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 191
DB 641 TGTGATGCTGTGAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 582
QY 192 TGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 233
DB 581 TCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540

RESULT 10
US-11-217-529-5627/c
Sequence 5627, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO

APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIRO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217, 529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5627
LENGTH: 1239
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-5627

Query Match 10.2%; Score 46.6; DB 7; Length 1239;
Best Local Similarity 50.7%; Pred. No. 2e-05;
Matches 112; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 21 TAAAGCTCAGAGATCTTCTTGTGAGCTTACTGCTGATATGCTGTGCTTACGTTCTTA 80
DB 1238 TACTGTGAGATGTTGCTGTGCTGCTGCAATGTTGACGCTGTGTGTGCTGTGCTGAT 1179
QY 81 CCAAGTTGTCCTGCTTACTGAGCTTCTGCACTTATCTGATGTTCAATGCACTTTC 140
DB 1178 TGGAGTTGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1119
QY 141 TGAACATCTGCTCCTGCTTCTGCTGCTTAAAGTTGAGAACAGAACCTGCTGTTTC 200
DB 1118 TGCAAGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1059
QY 201 TGTTCGTAAGCTGTTCAAGATGATCATATCGTTTGTG 241
DB 1058 GATTGGGCTTGGAGATTGAGATTGAGATTGCTGTGCTGTG 1018

RESULT 11
US-11-217-529-173524/c
Sequence 173524, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: KODAMA, NORIHISA
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIRO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217, 529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 173524
LENGTH: 159
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-173524

Query Match 10.1%; Score 46.2; DB 7; Length 159;
Best Local Similarity 57.1%; Pred. No. 9.6e-06;
Matches 84; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 61 GTTGCTGCTAAGCTTCTTAACCAAGTGTCCGTTACTAGAGCTTCTGCACTTATCTCT 120
DB 159 GTTGCTGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGCT 100
QY 121 GATGTCATACCTGCACTTCTGGAACATCTGCTCCTGCTTCTGTGCTTAAAGTTGAG 180


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RESULT 15
US-11-217-529-174534/c
; Sequence 174534, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174534
; LENGTH: 1368
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-174534

Query Match          9.3%; Score 42.8; DB 7; Length 1368;
Best Local Similarity 52.2%; Pred. No. 0.0003;
Matches 95; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 52 GCTGATATCGTTGCTGCTTACGTTTACCAAGCTTGTCCCTGTTACTGAGCTTCTGGA 111
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 586 GATGCTGTTGTTGCTGCTGTTGCTGTTGATGATGATGATGTTGTTGAAGTTGTT 527
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 112 CTTATCTGATGTTGATGATGACATTTCGGAACATCTGCTGCTGTTGTTGCTGTT 171
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 526 GTTGTGCAACTGCTGTTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGTT 467
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 172 AACGTTGAGAAGCAAGACCTGCTGTTCTGTTGTAAGTCTGTTTCAGATGATCATATC 231
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 466 GTATTTCAGACTGTTGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 407
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 232 GT 233
   ||
DB 406 GT 405

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Search completed: May 20, 2006, 01:28:01
 Job time : 20 secs